

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:37 ; Search time 18 Seconds
(without alignments)
85.453 Million cell updates/sec

Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNATFFYFKIDNVKKAR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	427	1 KGHUL1	kininogen, LMW pre
2	84	100.0	644	1 KGHUH1	kininogen, HMW pre
3	67	79.8	433	2 A28055	K-kininogen, LMW I
4	67	79.8	639	2 A25486	kininogen, HMW I p
5	59	70.2	434	1 KGBOL2	kininogen, LMW II
6	59	70.2	639	1 KGBOH2	kininogen, HMW II
7	56	66.7	423	1 KGR7M	major acute phase
8	56	66.7	430	1 KGR7T1	T-kininogen I prec
9	56	66.7	430	2 A23897	major acute phase
10	56	66.7	430	2 B28055	T-kininogen, LMW I
11	54	64.3	436	1 KGBOL1	kininogen, LMW I p
12	54	64.3	621	1 KGBOH1	kininogen, HMW I p
13	43	51.2	217	2 B97948	hypothetical prote
14	43	51.2	466	2 A81213	TN916 ORF21 homolo
15	42	50.0	657	2 B64791	hypothetical prote
16	41.5	49.4	469	2 F69403	hypothetical prote
17	41	48.8	454	2 G75105	hypothetical prote
18	41	48.8	895	2 T23191	hypothetical prote
19	41	48.8	996	2 F86410	protein F3M18.12 [
20	41	48.8	1007	2 T32285	hypothetical prote
21	41	48.8	1066	2 S72479	hypothetical prote
22	40.5	48.2	345	2 B97014	Nuc-2 protein - Ne
23	40	47.6	85	2 C90097	TPR-repeat-contain
24	40	47.6	179	2 A48474	hypothetical prote
25	40	47.6	333	2 B81356	icp18.5 homolog -
26	40	47.6	333	2 S77103	hypothetical prote
27	40	47.6	388	2 C95102	hypothetical prote
28	40	47.6	388	2 B97970	hypothetical prote
29	40	47.6	431	2 F89817	conserved hypothet

RESULT 1

KGHUL1

kininogen, LMW precursor [validated] - human

N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen

N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen

C:Species: Homo sapiens (man)

C>Date: 06-Jul-1982 #sequence.revision 27-Nov-1985 #text.change 08-Dec-2000

C:Accession: A01280; B25276; A27900; A27699; A31905; A34030

R:Okubo, I.; Kurachi, K.; Takasawa, T.; Shikawa, H.; Sasaki, M.

Biochemistry 23, 5691-5697, 1984

A:Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide

A:Reference number: A90490; MUID:85122621; PMID:6441591

A:Accession: A01280

A:Molecule type: mRNA

A:Residues: 1-427 <OHK>

A:Cross-references: GB:K02566; NID:g177889; PIDN:AAA35497.1; PID:g177890

R:Takagaki, Y.; Kitamura, N.; Nakanishi, S.

J. Biol. Chem. 260, 8601-8609, 1985

A:Title: Cloning and sequence analysis of cDNAs for human high molecular weight and 1

A:Reference number: A92544; MUID:85234582; PMID:2989293

A:Accession: B25276

A:Molecule type: mRNA

A:Residues: 1-427 <YAK>

A:Cross-references: GB:M11437; NID:g186751; PIDN:AAB59551.1; PID:g386853

R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Rauth, G.; Mueller-Esterl, W.

in Kinins IV, part A. Greenbaum, L.M., and Margolius, H.S., eds., pp.91-95, Plenum, N

A:Title: Amino acid sequence of the light chain of human low molecular mass kininogen

A:Reference number: A27900

A:Accession: A27900

A:Molecule type: protein

R:Mindrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.

Biochem. Biophys. Res. Commun. 152, 519-526, 1988

A:Title: A new kinin moiety in human plasma kininogens.

A:Reference number: A27699; MUID:88209021; PMID:3365237

A:Accession: A27699

A:Molecule type: protein

A:Residues: 380-389 <MIN>

R:Maeda, H.; Matsumura, Y.; Kato, H.

J. Biol. Chem. 263, 16051-16054, 1988

A:Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f

A:Reference number: A31905; MUID:89034061; PMID:3182782

A:Accession: A31905

A:Molecule type: protein

A:Residues: 381-389 <MAE>

R:Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.

Biochem. Biophys. Res. Commun. 150, 511-516, 1988

A:Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p

A:Reference number: A34030; MUID:88106632; PMID:3337729

A:Accession: A34030

A:Molecule type: protein

A:Residues: 380-389 <SAS>

R:Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 260, 8610-8617, 1985
 A:Title: Structural organization of the human kininogen gene and a model for its evolution
 A:Reference number: A92545; MUID:85234583; PMID:2989294
 A:Contents: annotation; gene organization
 R:Pierce, J.V.
 Fed. Proc. 27, 52-57, 1968
 A:Title: Structural features of plasma kinins and kininogens.
 A:Reference number: A91455; MUID:90255622; PMID:4952632
 A:Contents: annotation; bradykinin
 C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form (S)
 C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
 C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, 1
 xproline residue is present in the kininogen prior to the release of bradykinin.
 C:Genetics:
 A:Gene: GDB:KNG
 A:Cross-references: GDB:125256; OMIM:228960
 A:Map position: 3q27-3q27
 A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
 C:Superfamily: kininogen; cystatin homology
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; gly
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-427/Product: LMW prokininogen (kininogen I) #status predicted <MAT>
 F:19-389,390-427/Product: LMW kininogen II #status predicted <MAT>
 F:19-379/Product: LMW kininogen heavy chain #status predicted <HCN>
 F:19-131/Domain: cystatin homology <CYL>
 F:142-253/Domain: cystatin homology <CY2>
 F:264-375/Domain: cystatin homology <CV3>
 F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
 F:381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
 F:390-427/Product: LMW kininogen light chain #status experimental <LCH>
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:48-407,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/disulfide bonds:
 F:48,169,205,294/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
 F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 F:401/Binding site: carboxylate (Thr) (covalent) #status absent

Query Match 100.0%; Score 84; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 2.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFEKIDNVKKAR 16
 |||||||||
 Db 293 NNATFEKIDNVKKAR 308

RESULT 2
 KGHUHI
 Kininogen, HMW precursor [validated] - human
 N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
 N:Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular we
 C:Species: Homo sapiens (man)
 C:Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000
 C:Accession: A01279; A25276; S32422; A91153; A24871; A27899; A31905; A34030; S02
 R:Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiohara, H.; Sasaki, M.
 Biochemistry 23, 5691-5697, 1984
 A:Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identifi
 A:Reference number: A90490; MUID:85122621; PMID:6441591
 A:Accession: A01279
 A:Molecule type: mRNA
 A:Residues: 1-389 <OHK>
 A:Cross-references: GB:K02566; NID:gl77889
 R:Takagaki, Y.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A:Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
 A:Reference number: A92544; MUID:85234582; PMID:2989293
 A:Accession: A25276
 A:Molecule type: mRNA
 A:Residues: 1-592,1',594-644 <TAK>
 A:Cross-references: GB:M11437; NID:gl186751; PIDN:AA59550.1; PID:q386852
 R:Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.

FEBS Lett. 321, 93-97, 1993
 A:Title: Cloning, expression and characterization of human kininogen domain 3.
 A:Reference number: S32422; MUID:93223854; PMID:8467916
 A:Accession: S32422
 A:Molecule type: mRNA
 A:Residues: 'ANSK',253-377 <AUE>
 A:Note: differences are due to known cloning artifacts
 R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Foerisch, B.; Muller-Esterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A:Title: The amino acid sequence of the light chain of human high-molecular-mass k
 A:Reference number: A91153; MUID:86030270; PMID:4054110
 A:Accession: A91153
 A:Molecule type: protein
 A:Residues: 379-644 <LOT>
 A:Note: the bradykinin sequence preceding the light chain sequence was not determined
 R:Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
 Eur. J. Biochem. 154, 471-478, 1986
 A:Title: Completion of the primary structure of human high-molecular-mass kininogen.
 A:Reference number: A24871; MUID:86108361; PMID:3484703
 A:Accession: A24871
 A:Molecule type: protein
 A:Residues: 'Z',20-380 <KELL>
 R:Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
 in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New
 A:Title: Amino acid sequence of the light chain of human high molecular mass kininogen
 A:Reference number: A27899
 A:Accession: A27899
 A:Molecule type: protein
 A:Residues: 379-389, 'K',390-407, 'O',409-644 <KEL2>
 R:Mindroul, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
 Biochem. Biophys. Res. Commun. 152, 519-526, 1988
 A:Title: A new kinin moiety in human plasma kininogens.
 A:Reference number: A27699; MUID:88209021; PMID:3365237
 A:Accession: A27699
 A:Molecule type: protein
 A:Residues: 380-389 <MIN>
 R:Maeda, H.; Matsumura, Y.; Kato, H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A:Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
 A:Reference number: A31905; MUID:89034061; PMID:3182782
 A:Accession: A31905
 A:Molecule type: protein
 A:Residues: 381-389 <MAE>
 R:Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A:Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
 A:Reference number: A34030; MUID:88106632; PMID:3337729
 A:Accession: A34030
 A:Molecule type: protein
 A:Residues: 380-389 <SAS>
 R:Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A:Title: Human cathepsin B and cysteine proteinase inhibitors (CPis) in inflammatory
 A:Reference number: S02482; MUID:89076517; PMID:3264507
 A:Accession: S02482
 A:Molecule type: protein
 A:Residues: 1-19;189-192;310-314;381-389 <LENI>
 R:Kato, H.; Matsumura, Y.; Maeda, H.
 FEBS Lett. 232, 252-254, 1988
 A:Title: Isolation and identification of hydroxyproline analogues of bradykinin in hu
 A:Reference number: A61495; MUID:88211869; PMID:3366244
 A:Accession: A61495
 A:Molecule type: protein
 A:Residues: 380-389 <KAT1>
 A:Experimental source: urine
 A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A:Accession: B61495
 A:Molecule type: protein
 A:Residues: 381-389 <KAT2>
 A:Experimental source: urine
 A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A:Accession: C61495
 A:Molecule type: protein

A;Residues: 380-389 <KAT3>
R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A;Reference number: S14303; MUID:91192133; PMID:201314
A;Accession: S14447
A;Molecule type: protein
A;Residues: 264-359; N, 361-375 <LEN2>
R;Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity.
A;Reference number: S55239; MUID:95251593; PMID:7733867
A;Accession: S55239
A;Molecule type: protein
A;Residues: 450-452; X, 454, X, 456 <LIT>
R;Straczek, J.; Maachi, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabet, P.; Belleville, J.
FEBS Lett. 373, 207-211, 1995
A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like growth factor I release.
A;Reference number: S68059; MUID:96033974; PMID:7589467
A;Accession: S68059
A;Molecule type: protein
A;Residues: 431-434 <STR>
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evolution.
A;Reference number: A92545; MUID:85234583; PMID:2989294
A;Contents: annotation; gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455; MUID:90255622; PMID:4952632
A;Contents: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene.
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the blood coagulation.
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is important for its biological activity.
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, and its release is regulated by the kininogen prior to the release of bradykinin.
C;Genetics:
A;Gene: GDB:KNG
A;Cross-references: GDB:125256; OMIM:228960
A;Map position: 3q27-3q27
A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duplication
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379/Product: HMW kininogen II (prokininogen) #status experimental <MAT2>
F;19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F;19-131/Domain: HMW kininogen heavy chain #status experimental <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
F;390-644/Domain: HMW kininogen light chain #status experimental <LCH>
F;421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F;431-434/Product: low molecular weight growth promoting factor #status experimental <GH>
F;19/Modified site: pyroglutamic carboxylic acid (Gln) (in mature form) #status experimental
F;28-614, 83-94, 107-142, 145, 206-218, 229-248, 264-267, 328-340, 351-370/Disulfide bonds:
F;48/Binding site: carboxylate (Asn) (covalent) #status absent
F;169-205, 294/Binding site: carboxylate (Asn) (covalent) #status experimental
F;379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F;383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;401-533, 542, 546, 557, 571, 593, 628/Binding site: carboxylate (Thr) (covalent) #status experimental
F;577/Binding site: carboxylate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 84; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 16
Db 293 NNATFFFKIDNVKKA 308

RESULT 3

A28055
K-kininogen, LMW I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
C;Accession: A28055
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.
A;Reference number: A92496; MUID:86008264; PMID:2413018
A;Accession: A28055
A;Molecule type: mRNA
A;Residues: 1-433 <FUR>
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-433/Product: K-kininogen, LMW I #status predicted <MAT>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>

Query Match 79.8%; Score 67; DB 2; Length 433;
Best Local Similarity 86.7%; Pred. No. 0.002;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
Db 293 NNATFFFKIDNVKKA 307

RESULT 4

A25486
kininogen, HMW I precursor - rat
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number: A92625; MUID:87137443; PMID:3029068
A;Accession: A25486
A;Molecule type: mRNA
A;Residues: 1-639 <KIT>
A;Note: the authors translated the codon CAA for residue 347 as Asn
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-639/Product: kininogen, HMW I #status predicted <MAT>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>

Query Match 79.8%; Score 67; DB 2; Length 639;
Best Local Similarity 86.7%; Pred. No. 0.0029;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
Db 293 NNATFFFKIDNVKKA 307

RESULT 5

KB0L2
kininogen, LMW II precursor - bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
C;Accession: A01284

R:Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
 Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
 A:Title: Primary structures of bovine liver low molecular weight kininogen precursors and
 A:Reference number: A93984; MUID:83117859; PMID:6572010
 A:Accession: A01284
 A:Molecule type: mRNA
 A:Residues: 1-434 <NAN>
 A:CROSS-references: GB:V00427; GB:J00011; NID:g489; PIDN:CAA23710.1; PID:g490
 C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form as
 C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
 C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, a
 C:Superfamily: kininogen; cystatin homology
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyco
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-434/Product: LMW kininogen II #status predicted <MAT>
 F:19-377/Product: LMW kininogen I heavy chain #status predicted <HCH>
 F:19-130/Domain: cystatin homology <CY1>
 F:141-252/Domain: cystatin homology <CY2>
 F:261-372/Domain: cystatin homology <CY3>
 F:377-386/Product: lysyl-bradykinin (kallidin II) #status predicted <KB DY>
 F:378-386/Product: bradykinin (kallidin I) #status predicted <BDY>
 F:387-434/Product: LMW kininogen I light chain #status experimental <LCH>
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:27-404,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
 F:47,87,168,169,197,204,280/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:376-377/Cleavage site: Met-Lys (kallikrein) #status predicted
 F:380/Modified site: 4-hydroxyproline (Pro) #status predicted
 F:386-387/Cleavage site: Arg-Ser (kallikrein) #status predicted
 Query Match 70.2%; Score 59; DB 1; Length 434;
 Best Local Similarity 73.3%; Pred. No. 0.043; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 11; Conservative 2;
 Qy 1 NNATFFYKIDNVKKA 15
 Db 290 HDGTFYKIDNVKKA 304
 RESULT 6
 KGBOH2
 N:kininogen, HMW II precursor - bovine
 N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
 N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
 C:Accession: A01282; A91923; A91941; A91938; B29559
 R:Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
 Nature 305, 545-549, 1983
 A:Title: A single gene for bovine high molecular weight and low molecular weight kininogen
 A:Reference number: A93317; MUID:84014106; PMID:6571699
 A:Accession: A01282
 A:Molecule type: mRNA
 A:Residues: 1-619 <KIT>
 A:CROSS-references: GB:V01492; GB:K01758; NID:g493; PIDN:CAA24736.1; PID:g494
 R:Kato, H.; Nagasawa, S.; Suzuki, T.
 J. Biochem. 67, 313-323, 1970
 A:Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
 A:Reference number: A91923; MUID:70180420; PMID:4986212
 A:Accession: A91923
 A:Molecule type: protein
 A:Residues: 376-391 <KAT>
 R:Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.
 J. Biochem. 79, 1201-1222, 1976
 A:Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino a
 A:Reference number: A91941; MUID:76260155; PMID:956151
 A:Accession: A91941
 A:Molecule type: protein
 A:Residues: 387-455 <HAN>
 A:Note: 398-Pro, 401-Val, and 455-Lys were also found
 R:Han, Y.N.; Komiyama, M.; Iwanaga, S.; Suzuki, T.
 J. Biochem. 77, 55-68, 1975
 A:Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Am

A:Reference number: A91938; MUID:75170265; PMID:1169237
 A:Accession: A91938
 A:Molecule type: protein
 A:Residues: 456-456 <HA2>
 R:Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwana
 J. Biol. Chem. 262, 2768-2779, 1987
 A:Title: Bovine high molecular weight kininogen. The amino acid sequence, positions o
 A:Reference number: A92627; MUID:87137530; PMID:3546295
 A:Accession: B29559
 A:Molecule type: protein
 A:Residues: 'Z', 20-104, 'E', 106-256, 'XX', 257-376 <SUB>
 R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Foerisch, B.; Muller-Esterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A:Title: The amino acid sequence of the light chain of human high-molecular-mass kini
 A:Reference number: A91153; MUID:86030270; PMID:4054110
 C:Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
 R:Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
 Seikagaku 56, 808, 1984
 A:Title: Disulfide bonds in bovine HMW kininogens.
 A:Reference number: A94300
 A:Contents: annotation; disulfide bonds
 A:Note: article in Japanese
 C:Comment: The HMW kininogen precursor is produced from the same gene as the LMW form
 C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of
 C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is i
 C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
 C:Comment: xproline residue is present in the kininogen prior to the release of bradykinin.
 C:Superfamily: kininogen; cystatin homology
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-619/Product: HMW kininogen II #status predicted <MAT>
 F:19-376/Product: HMW kininogen II heavy chain #status experimental <HCH>
 F:19-130/Domain: cystatin homology <CY1>
 F:141-252/Domain: cystatin homology <CY2>
 F:261-372/Domain: cystatin homology <CY3>
 F:377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KB DY>
 F:378-386/Product: bradykinin (kallidin I) #status experimental <BDY>
 F:387-619/Product: HMW kininogen II light chain #status experimental <LCH>
 F:418-488/Region: glycine/histidine/lysine-rich
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
 F:27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bond
 F:47/Binding site: carboxylate (Asn) (covalent) #status absent
 F:87,168,169,204,280/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:136/Binding site: carboxylate (Thr) (covalent) (partial) #status experimental
 F:197/Binding site: carboxylate (Asn) (covalent) (partial) #status experimental
 F:376-377/Cleavage site: Met-Lys (kallikrein) #status experimental
 F:380/Modified site: 4-hydroxyproline (Pro) #status predicted
 F:386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental
 F:396,400,404,510/Binding site: carboxylate (Ser) (covalent) #status experimental
 F:397,398,518,522,534,546,551,568/Binding site: carboxylate (Thr) (covalent) #status
 F:496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental
 Query Match 70.2%; Score 59; DB 1; Length 619;
 Best Local Similarity 73.3%; Pred. No. 0.061; 2; Mismatches 2; Indels 0; Gaps 0;
 Matches 11; Conservative 2;
 Qy 1 NNATFFYKIDNVKKA 15
 Db 290 HDGTFYKIDNVKKA 304
 RESULT 7
 KGRTM
 N:acute phase alpha-1 protein precursor - rat (fragment)
 N:Contains: bradykinin
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
 C:Accession: A01285
 R:Cole, T.; Inglis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
 FEBS Lett. 182, 57-61, 1985
 A:Title: Major acute phase alpha1-protein of the rat is homologous to bovine kininoge
 A:Reference number: A01285; MUID:65127561; PMID:2578992
 A:Accession: A01285

A:Molecule type: mRNA
A:Residues: 1-423 <COL>
C:Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflammation.
R:
C:Superfamily: kininogen; cystatin homology
C:Keywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflammation
F;1-11/Domain: signal sequence (fragment) #status predicted <SIG>
F;12-423/Product: major acute phase alpha-1 protein #status predicted <MAT>
F;12-123/Domain: cystatin homology <CY1>
F;134-245/Domain: cystatin homology <CY2>
F;256-367/Domain: cystatin homology <CY3>
F;371-379/Product: bradykinin #status predicted <BDY>
F;12/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;161,197/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 66.7%; Score 56; DB 1; Length 423;
Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
: | ||||| ||||
Db 285 HNHFFFKIDTVKKA 299

RESULT 8
KGRFT1
T-kininogen I precursor - rat
N:Alternate names: 73K protein; LMW kininogen T-I
N:Contains: bradykinin; T-kinin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C:Accession: A01286; D25486; A28526; PLO193; JQ0027; B25488; A28525; S68036
R:Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.
A:Reference number: A92496; MUID:86008264; PMID:2413018
A:Accession: A01286
A:Molecule type: mRNA
A:Residues: 1-430 <FUR>
R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A:Title: Differing expression patterns and evolution of the rat kininogen gene family.
A:Reference number: A92625; MUID:87137443; PMID:3029068
A:Accession: D25486
A:Molecule type: DNA
A:Residues: 375-430 <KTR>
R:Enyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A:Title: Purification and characterization of rat T-kininogens isolated from plasma of a
A:Reference number: A92729; MUID:88087226; PMID:3121623
A:Accession: A28526
A:Molecule type: protein
A:Residues: 16,20-48;376-430 <EN>
R:Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiya, S.; Tomino, S.; Nagase, S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A:Title: Identification of a protein increasing in serum of Nagase analbuminemic rats be
A:Reference number: PLO193; MUID:90216390; PMID:2108948
A:Accession: PLO193
A:Molecule type: mRNA
A:Residues: 330-420,'R',422-429,'P' <KAN>
R:Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A:Title: Primary structure of a gene encoding rat T-kininogen.
A:Reference number: JQ0027; MUID:90034172; PMID:2806908
A:Accession: JQ0027
A:Molecule type: DNA
A:Residues: 1-60,'E',62-113,'R',115-165,'F',167-178,'TKI',182-211,'F',213-256,'S',258-38
A:Experimental source: strain Sprague-Dawley
R:Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A:Title: Differing utilization of homologous transcription initiation sites of rat K and

A:Reference number: A25488; MUID:87137465; PMID:3818598
A:Accession: B25488
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-48 <KAG>
A:Cross-references: GB:M14356; NID:g205090; PIDN:AAA41492.1; PID:g205091
R:Enyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 965-972, 1988
A:Title: Purification and characterization of two kinds of low molecular weight kinin
A:Reference number: A28525; MUID:88087225; PMID:3335530
A:Accession: A28525
A:Molecule type: protein
A:Residues: 376-430 <EN>
R:Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A:Title: Identification of several isoforms of T-kininogen expressed in the liver of
A:Reference number: S68034; MUID:96032652; PMID:7574705
A:Accession: S68036
A:Molecule type: mRNA
A:Residues: 340-430 <SIE>
A:Experimental source: clone pSG17
C:Comment: At least three types of LMW kininogen precursors are present in rat plasma
ceding bradykinin.
C:Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after
d of an Arg or Lys, it is probably not released from its precursor by either tissue o
C:Comment: The T-kininogens are produced in response to an inflammatory stimulant.
C:Genetics:
A:Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
C:Superfamily: kininogen; cystatin homology
C:Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; gly
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-430/Product: T-kininogen I #status experimental <MAT>
F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>
F;378-386/Product: bradykinin #status predicted <BDY>
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
F;82,126,168,204,326/Binding site: carboxylate (Asn) (covalent) #status predicted
F;83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #sta

Query Match 66.7%; Score 56; DB 1; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
: | ||||| ||||
Db 292 HNHFFFKIDTVKKA 306

RESULT 9
A23897
major acute phase alpha-1 protein (version 2) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C:Accession: A23897; B23897
R:Anderson, K.P.; Heath, E.C.
J. Biol. Chem. 260, 12065-12071, 1985
A:Title: The relationship between rat major acute phase protein and the kininogens.
A:Reference number: A23897; MUID:86008266; PMID:2413019
A:Accession: A23897
A:Molecule type: protein
A:Residues: 1-14 <AND1>
A:Accession: B23897
A:Molecule type: mRNA
A:Residues: 5-430 <AND2>
A:Cross-references: GB:M11661; NID:g205307; PIDN:AAA41570.1; PID:g205308
A:Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue
C:Superfamily: kininogen; cystatin homology
F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>

Query Match 66.7%; Score 56; DB 2; Length 430;

Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
: | | | | | | | | | |
Db 292 HNHLEFYFKIDTVKKA 306

RESULT 10

B28055
T:kininogen, LMW II precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 12-Dec-1997
C:Accession: B28055; E25486; B28526
R:Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.
A:Reference number: A92496; MUID:86008264; PMID:2413018
A:Accession: B28055
A:Molecule type: mRNA
A:Residues: 1-430 <P>
R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A:Title: Differing expression patterns and evolution of the rat kininogen gene family.
A:Reference number: A92625; MUID:87137443; PMID:3029068
A:Accession: E25486
A:Molecule type: DNA
A:Residues: 375-430 <KIT>
R:Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A:Title: Purification and characterization of rat T-kininogens isolated from plasma of a
A:Reference number: A92729; MUID:88087226; PMID:3121623
A:Accession: B28526
A:Molecule type: protein
A:Residues: 'E', 20-25, 'MD', 28-48, 376-430 <ENJ>
A:Accession: C28526
A:Molecule type: protein
A:Residues: 'E', 20-48; 376-388, 'R', 390-419, 'ER', 422-430 <ENJ>
C:Superfamily: kininogen; cystatin homology
C:Keywords: glycoprotein; pyroglutamic acid
F:1-18/Domain: signal sequence, LMW II #status experimental <SIG>
F:19-430/Product: T-kininogen, LMW II #status experimental <MAT>
F:19-130/Domain: cystatin homology <CY1>
F:141-252/Domain: cystatin homology <CY2>
F:263-374/Domain: cystatin homology <CY3>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:82,126,168,204,326/Binding site: carboxylate (Asn) (covalent) #status predicted
F:83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status

Query Match 66.7%; Score 56; DB 2; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
: | | | | | | | | | |
Db 292 HNHLEFYFKIDTVKKA 306

RESULT 11

KGB011
kininogen, LMW I precursor - bovine
N:Alternate names: alpha-2-thiol proteinase inhibitor; prokininogen
N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C:Accession: A01283
R:Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A:Title: Primary structures of bovine liver low molecular weight kininogen precursors and
A:Reference number: A93984; MUID:83117859; PMID:6572010
A:Accession: A01283
A:Molecule type: mRNA

A:Residues: 1-436 <N>
A:Cross-references: GB:J00010; GB:V00426; NID:g163256; PIDN:AAA30604.1; PID:g163257
C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of
C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
xyproline residue is present in the kininogen prior to the release of bradykinin.
C:Superfamily: kininogen; cystatin homology
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; g
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-436/Product: LMW kininogen I #status predicted <MAT>
F:19-378/Product: LMW kininogen I heavy chain #status predicted <HCH>
F:19-130/Domain: cystatin homology <CY1>
F:141-252/Domain: cystatin homology <CY2>
F:263-374/Domain: cystatin homology <CY3>
F:379-388/Product: lysyl-bradykinin (kallidin I) #status predicted <KBDY>
F:380-436/Product: bradykinin (kallidin I) #status predicted <BDY>
F:389-436/Product: LMW kininogen I light chain #status experimental <LCH>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:27-406,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bond
F:47,87,168,169,197,204/Binding site: carboxylate (Asn) (covalent) #status predicted
F:378-379/Cleavage site: Met-Lys (kallikrein) #status predicted
F:382/Modified site: 4-hydroxyproline (Pro) #status predicted
F:388-389/Cleavage site: Arg-Ser (kallikrein) #status predicted
Query Match 64.3%; Score 54; DB 1; Length 436;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
: | | | | | | | | | |
Db 292 HDGAFFFKIDTVKKA 306

RESULT 12
KGB011
kininogen, HMW I precursor - bovine
N:Alternate names: alpha-2-thiol proteinase inhibitor; prokininogen
N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C:Accession: A01281; A91923; A91938; A29559
R:Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
Nature 305, 545-549, 1983
A:Title: A single gene for bovine high molecular weight and low molecular weight kinin
A:Reference number: A93317; MUID:84014106; PMID:6571699
A:Accession: A01281
A:Molecule type: mRNA
A:Residues: 1-621 <KIT>
A:Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1; PID:g492
R:Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
A:Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds a
A:Reference number: A91923; MUID:70180420; PMID:4986212
A:Accession: A91923
A:Molecule type: protein
A:Residues: 378-393 <KAT>
R:Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.
J. Biochem. 77, 55-68, 1975
A:Title: Studies on the primary structure of bovine high-molecular-weight kininogen.
A:Reference number: A91938; MUID:75170265; PMID:1169237
A:Accession: A91938
A:Molecule type: protein
A:Residues: 458-498 <HAN>
R:Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwana
J. Biol. Chem. 262, 2768-2779, 1987
A:Title: Bovine high molecular weight kininogen. The amino acid sequence, positions o
A:Reference number: A92627; MUID:87137530; PMID:3546295
A:Accession: A29559
A:Molecule type: protein
A:Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 <SUE>
R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A:Title: The amino acid sequence of the light chain of human high-molecular-mass kinin

Db 33>NNLLFYSKFYNIKSRR 48

RESULT 14

AH1213

TN916 ORF21 homolog lmoll12 [imported] - *Listeria monocytogenes* (strain EGD-e)

C:Species: *Listeria monocytogenes*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AH1213

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A:Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AH1213

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-466 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAC99190.1; PID:gl6410514; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmoll12

Query Match 51.2%; Score 43; DB 2; Length 466;
Best Local Similarity 60.0%; Pred No. 22;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Caps 0;

QY 5 FYFKIDNVKK 14
:|||||:

Db 85 YYKIDNIKQ 94

RESULT 15

B84791

hypothetical protein At2g37310 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001

C:Accession: B84791

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84791

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-657 <STO>

A:Cross-references: GB:AE002093; NID:g4056485; PIDN:AAC98051.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g37310

A:Map position: 2

C:Superfamily: *Arabidopsis thaliana* hypothetical protein T8H10.30

Query Match 50.0%; Score 42; DB 2; Length 657;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Caps 0;

QY 4 TFYFKIDNVKKAR 16
|:| | | | | | |

Db 175 TTYTKCDNIKSAR 187

Search completed: March 13, 2003, 19:14:02

Job time : 19 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:02 ; Search time 10 Seconds
(without alignments)
66.362 Million cell updates/sec

Title: US-09-461-061A-10

Perfect score: 84

Sequence: 1 NNATFFKIDNVKKAR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	644	1 KNG_HUMAN	P01042 homo sapien
2	67	79.8	639	1 KNG_RAT	P08934 rattus norv
3	59	70.2	434	1 KNL2_BOVIN	P01047 bos taurus
4	59	70.2	619	1 KNL2_BOVIN	P01048 rattus norv
5	56	66.7	430	1 KNT1_RAT	P08932 rattus norv
6	56	66.7	430	1 KNT2_RAT	P01046 bos taurus
7	54	64.3	436	1 KNL1_BOVIN	P01044 bos taurus
8	54	64.3	621	1 KNL1_BOVIN	P01044 bos taurus
9	53	63.1	661	1 KNG_MOUSE	P08677 mus musculu
10	41	48.8	208	1 LEUD_BUCDN	O85073 buchnera ap
11	41	48.8	1066	1 NUC2_NEUCR	Q01317 neurospora
12	39	46.4	237	1 YS76_CAEEL	Q09619 caenorhabdi
13	39	46.4	306	1 YDS4_SCHPO	O14180 schizosacch
14	39	46.4	406	1 HELK_BUCAI	P57631 buchnera ap
15	38	45.2	224	1 KCY_UREPA	Q9pqe9 ureaplasma
16	38	45.2	297	1 YDC1_SCHPO	Q10422 schizosacch
17	38	45.2	312	1 TRUB_BUCAI	P57456 buchnera ap
18	38	45.2	316	1 UFD1_DROME	Q9vtf9 drosophila
19	38	45.2	513	1 PPT1_YEAST	P53043 saccharomyc
20	37	44.0	219	1 Y413_RICPR	P93db9 rickettsia
21	37	44.0	256	1 PXBB_CANBO	Q00317 candida bol
22	37	44.0	316	1 VSH5_DICDI	P14326 dictyosteli
23	37	44.0	365	1 OMLA_ACTPL	Q02937 actinobacil
24	37	44.0	384	1 YXT2_YEAST	P03879 saccharomyc
25	37	44.0	452	1 PLM1_PLAFA	P39898 plasmodium
26	37	44.0	470	1 YC82_RICPR	Q9zct8 rickettsia
27	37	44.0	516	1 YC82_EUGGR	P30397 euglena gra
28	37	44.0	550	1 DBP2_SCHPO	P24782 schizosacch
29	37	44.0	738	1 ST11_YEAST	P23561 saccharomyc
30	37	44.0	1816	1 KF1B_MOUSE	Q60575 mus musculu
31	36.5	43.5	403	1 YA24_METJA	Q58430 methanococ
32	36.5	43.5	514	1 GUXC_FUSOX	P46238 fusarium ox
33	36	42.9	80	1 BMP3_BOVIN	P22444 bos taurus

ALIGNMENTS

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RESULT 1
KNG_HUMAN
ID KNG_HUMAN STANDARD; PRT; 644 AA.
AC P01042; P01043;
DT 21-JUL-1986 (Rel. 01, Created)
; DT 01-FEB-1996 (Rel. 33, Last sequence update)
; DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kininogen precursor (Alpha-2-thiol proteinase inhibitor) [Contains:
DE Bradykinin].
GN KNG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
RX MEDLINE=85234582; PubMed=2989293;
RA Takagaki Y., Kitamura N., Nakanishi S.;
RT "Cloning and sequence analysis of cDNAs for human high molecular
RT weight and low molecular weight prekininogens. Primary structures of
RT two human prekininogens."
RL J. Biol. Chem. 260:8601-8609(1985).
RN [2]
RP GENE STRUCTURE
RX MEDLINE=85234583; PubMed=2989294;
RA Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T.,
RA Nakanishi S.;
RT "Structural organization of the human kininogen gene and a model for
RT its evolution."
RL J. Biol. Chem. 260:8610-8617(1985).
RN [3]
RP SEQUENCE OF 1-401 FROM N.A.
RX MEDLINE=85122621; PubMed=6441591;
RA Ohkubo I., Kurachi K., Takasawa T., Shiohawa H., Sasaki M.;
RT "Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and
RT its identity with low molecular weight kininogen."
RL Biochemistry 23:5691-5697(1984).
RN [4]
RP SEQUENCE OF 379-644.
RX MEDLINE=86030270; PubMed=4054110;
RA Lottspeich F., Kellermann J., Henschen A., Foertsch B.,
RA Mueller-Esterl W.;
RT "The amino acid sequence of the light chain of human high-molecular-
RT mass kininogen."
RL Eur. J. Biochem. 152:307-314(1985).
RN [5]
RP SEQUENCE OF 381-389.
RX MEDLINE=90255622; PubMed=4952632;
RA Pierce J.V.;
RT "Structural features of plasma kinins and kininogens."
RL Fed. Proc. 27:52-57(1968).
RN [6]
RP DISULFIDE BONDS.
RA Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
RT "Disulfide bonds in bovine HMW kininogens."

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P45477 haemophilus
P31765 haemophilus
O01258 caenorhabdi
P57531 buchnera ap
P40902 schizosacch
Q49573 mycoplasma
P55110 legionella
P32367 saccharomyc
P09952 micrococcus
P23980 lycopersico
P09798 saccharomyc
O76332 oxytricha t

RT "Primary structures of the mRNAs encoding the rat precursors for
 RT bradykinin and T-kinin. Structural relationship of kininogens with
 RT major acute phase protein and alpha 1-cysteine proteinase
 RL inhibitor.";
 RL J. Biol. Chem. 260:12054-12059(1985).
 RN [3]
 RP SEQUENCE OF 1-65 FROM N.A.
 RC STRAIN=Buffalo;
 RX MEDLINE=87250580; PubMed=2439509;
 RA Fung W.-P., Schreiber G.;
 RT "Structure and expression of the genes for major acute phase alpha 1-
 RT protein (thiostatin) and kininogen in the rat.";
 RL J. Biol. Chem. 262:9298-9308(1987).
 RN [4]
 RP SEQUENCE OF 1-41 FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=87137465; PubMed=3818598;
 RA Kageyama R., Kitamura N., Okubo H., Nakanishi S.;
 RT "Differing utilization of homologous transcription initiation sites
 RT of rat K and T kininogen genes under inflammation condition.";
 RL J. Biol. Chem. 262:2345-2351(1987).
 CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOLE PROTEASES; (2)
 CC HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
 CC HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
 CC FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
 CC INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
 CC BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF
 CC PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
 CC CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
 CC DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
 CC MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
 CC PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
 CC OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
 CC A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
 CC INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5)
 CC LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-
 CC KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
 CC CLOTTING.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
 CC -1- MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL
 CC HMW/LMW KININOGENS AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I AND
 CC T-II.
 CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
 CC -----
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 DR ENBL; L29428; AAA41486.1; -;
 DR ENBL; M11884; AAA41487.1; -;
 DR ENBL; M14369; AAA41484.1; -;
 DR ENBL; M14369; AAA41485.1; -;
 DR ENBL; M16455; AAA41482.1; -;
 DR PIR; A25486; A25486.
 DR PIR; A28055; A28055.
 DR InterPro; IPR000010; Cystatin.
 DR InterPro; IPR002395; Kininogen.
 DR Pfam; PF00031; cystatin; 3.
 DR PRINTS; PR00334; KININOGEN.
 DR SMART; SM00043; CY; 3.
 DR PROSITE; PS00287; CYSTATIN; 2.
 KW Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
 KW Bradykinin; Blood coagulation; Inflammatory response; Signal;
 KW Alternative splicing; Multigene family.
 FT SIGNAL 1 18

FT	CHAIN	19	639	KININOGEN.
FT	CHAIN	19	380	KININOGEN HEAVY CHAIN.
FT	PEPTIDE	381	389	BRADYKININ.
FT	CHAIN	390	639	KININOGEN LIGHT CHAIN.
FT	DOMAIN	19	136	CYSTATIN-LIKE 1.
FT	DOMAIN	137	258	CYSTATIN-LIKE 2.
FT	DOMAIN	259	380	CYSTATIN-LIKE 3.
FT	DOMAIN	439	514	HIS-RICH.
FT	DISULFID	28	609	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	83	94	BY SIMILARITY.
FT	DISULFID	107	126	BY SIMILARITY.
FT	DISULFID	142	145	BY SIMILARITY.
FT	DISULFID	206	218	BY SIMILARITY.
FT	DISULFID	229	248	BY SIMILARITY.
FT	DISULFID	264	267	BY SIMILARITY.
FT	DISULFID	328	340	BY SIMILARITY.
FT	DISULFID	351	370	BY SIMILARITY.
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	127	127	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	529	529	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	402	433	VPSYIARVQEDPDGNEQPIHGHGWLHAKQ -> RLIMS
FT				CEYGRLLKAGAPAPERQAEASTVTP (IN ISOFORM
FT				LMW).
FT	VARSPPLIC	434	639	MISSING (IN ISOFORM LMW).
FT	CONFLICT	61	61	E -> K (IN REF. 2).
FT	SEQUENCE	639 AA; 70933 MW;		D3172DF94FF56AF5 CRC64;

Query Match 79.8%; Score 67; DB 1; Length 639;
 Best Local Similarity 86.7%; Pred. No. 0.00095;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	NNATFFFKIDNVKKA	15
	11		1111
DB	293	NNHTFFFKIDTVKKA	307

RESULT 3
 KNL2_BOVIN STANDARD; PRT; 434 AA.
 ID KNL2_BOVIN
 AC P01047;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Kininogen, LMW II precursor (Thiol proteinase inhibitor) [Contains:
 DE Bradykinin].
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=83117859; PubMed=6572010;
 RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
 RT "Primary structures of bovine liver low molecular weight kininogen
 RT precursors and their two mRNAs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
 RN [2]
 RP SEQUENCE OF 19-376.
 RX MEDLINE=87137530; PubMed=3546295;
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
 RA Miyata T., Iwanaga S.;
 RT "Bovine high molecular weight kininogen. The amino acid sequence,
 RT positions of carbohydrate chains and disulfide bridges in the heavy
 RT chain portion.";
 RL J. Biol. Chem. 262:2768-2779(1987).
 CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOLE PROTEASES; (2)
 CC LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
 CC ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LMW-KININOGEN SHOWS
 CC A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH

CC MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)
CC NADRIURESIS AND DIURESIS (KIDNEY).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; LMW II (shown here) and HMW II
CC (AC P01045); are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
CC -1- MISCELLANEOUS: LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
CC INVOLVED IN BLOOD CLOTTING.
CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; V00427; CAA23710.1; -
DR PIR; A01284; KGBOL2.
DR HSP; P01038; 1A90.
DR InterPro: IPR000010; Cystatin.
DR Pfam: PF00031; cystatin; 3.
DR SMART; SM00043; C1; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
KW Thiol protease inhibitor; Bradykinin; Signal.
FT SIGNAL 1 18
FT CHAIN 19 434 KININOGEN, LMW II.
FT CHAIN 19 376 HEAVY CHAIN.
FT PEPTIDE 378 386 BRADYKININ.
FT CHAIN 387 434 LIGHT CHAIN.
FT DOMAIN 19 135 CYSTATIN-LIKE 1.
FT DOMAIN 136 256 CYSTATIN-LIKE 2.
FT DOMAIN 257 376 CYSTATIN-LIKE 3.
FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .).
FT CARBOHYD 136 136 O-LINKED (PARTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .); OR 169.
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (PARTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).
FT DISULFID 27 404 INTERCHAIN.
FT DISULFID 82 93
FT DISULFID 106 125
FT DISULFID 141 144
FT DISULFID 205 217
FT DISULFID 228 247
FT DISULFID 261 264
FT DISULFID 325 337
FT DISULFID 348 367
SQ SEQUENCE 434 AA; 73A0709DE3E03430 CRC64;
Query Match 70.2%; Score 59; DB 1; Length 434;
Best Local Similarity 73.3%; Pred. No. 0.014;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 NNATFFYKIDNVKKA 15
DB 290 HDGTFYKIDNVKKA 304
:: ||||| ||||
RESULT 4
ID KNH2_BOVIN STANDARD; PRT; 619 AA.
AC P01045.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kininogen, HMW II precursor (Thiol proteinase inhibitor) [Contains:
DE Bradykinin].
OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84014106; PubMed=6571699;
RA Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
RT "A single gene for bovine high molecular weight and low molecular
RT weight kininogens.";
RL Nature 305:545-549(1983).
RN [2]
RP SEQUENCE OF 19-376.
RX MEDLINE=87137530; PubMed=3546295;
RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA Miyata T., Iwanaga S.;
RT "Bovine high molecular weight kininogen. The amino acid sequence,
RT positions of carbohydrate chains and disulfide bridges in the heavy
RT chain portion.";
RL J. Biol. Chem. 262:2768-2779(1987).
RN [3]
RP SEQUENCE OF 376-391.
RX MEDLINE=70180420; PubMed=4986212;
RA Kato H., Nagasawa S., Suzuki T.;
RT "Studies on the structure of bovine kininogen: cleavages of disulfide
RT bonds and of methionyl bonds in kininogen-II.";
RL J. Biochem. 67:313-323(1970).
RN [4]
RP SEQUENCE OF 387-455.
RX MEDLINE=76260155; PubMed=956151;
RA Han Y.N., Kato H., Iwanaga S., Suzuki T.;
RT "Primary structure of bovine plasma high-molecular-weight kininogen.
RT The amino acid sequence of a glycopeptide portion (fragment 1)
RT following the C-terminus of the bradykinin moiety.";
RL J. Biochem. 79:1201-1222(1976).
RN [5]
RP SEQUENCE OF 456-496.
RX MEDLINE=75170265; PubMed=1169237;
RA Han Y.N., Komiyama M., Iwanaga S., Suzuki T.;
RT "Studies on the primary structure of bovine high-molecular-weight
RT kininogen. Amino acid sequence of a fragment ('histidine-rich
RT peptide') released by plasma kallikrein.";
RL J. Biochem. 77:55-68(1975).
CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOLE PROTEASES; (2)
CC HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
CC HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XII NEXT
CC TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND
CC PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE
CC PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS
CC A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
CC MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
CC NADRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
CC (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
CC IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
CC RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
CC (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
CC ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
CC ACTION).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; HMW II (shown here) and LMW II
CC (AC P01047); are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
CC -----
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DR EMBL; V01492; CAA24736.1; -.
DR EMBL; V01492; CAA24737.1; ALT_SEQ.
DR PIR; A01282; KGBOR2.
DR PIR; B29559; B29559.
DR HSP; P01038; 1A90.
DR InterPro; IPR000010; Cystatin.
DR InterPro; IPR002395; Kininogen.
DR Pfam; PF00031; cystatin; 3.
DR PRINTS; PR00334; KININOGEN.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
KW Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
KW Inflammatory response.
FT SIGNAL 1 18
FT CHAIN 19 619 KININOGEN, HMW II.
FT CHAIN 19 376 HEAVY CHAIN.
FT PEPTIDE 378 386 BRADYKININ.
FT CHAIN 387 619 LIGHT CHAIN.
FT DOMAIN 19 135 CYSTATIN-LIKE 1.
FT DOMAIN 136 256 CYSTATIN-LIKE 2.
FT DOMAIN 257 376 CYSTATIN-LIKE 3.
FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .).
FT CARBOHYD 136 136 O-LINKED (PARTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .); OR 169.
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (PARTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).
FT CARBOHYD 400 400 O-LINKED.
FT DISULFID 27 589 INTERCHAIN.
FT DISULFID 82 93
FT DISULFID 106 125
FT DISULFID 141 144
FT DISULFID 205 217
FT DISULFID 228 247
FT DISULFID 261 264
FT DISULFID 325 337
FT DISULFID 348 367
FT VARIANT 398 398
FT VARIANT 401 401 T -> P.
FT VARIANT 454 454 L -> V.
FT VARIANT 454 454 H -> K.
SQ SEQUENCE 619 AA; 68710 MW; F04320A8EB0E0DA CRC64;

Query Match 70.2%; Score 59; DB 1; Length 619;
Best Local Similarity 73.3%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
DB 290 HDSTFFFKIDTVKKA 304
:: ||||| ||||

RESULT 5
KNT1_RAT
ID KNT1_RAT STANDARD; PRT; 430 AA.
AC P01048; P04081;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-kininogen I precursor (Major acute phase protein) (Alpha-1-MAP)
DE (Thiostatin) [Contains: T-kinin].
GN MAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE-86008264; PubMed-2413018;
RA Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT "Primary structures of the mRNAs encoding the rat precursors for
bradykinin and T-kinin. Structural relationship of kininogens with
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RT major acute phase protein and alpha 1-cysteine proteinase
RT inhibitor.";
RL J. Biol. Chem. 260:12054-12059(1985).
RN [2]
RP SEQUENCE OF 5-430 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-86008266; PubMed-2413019;
RA Anderson K.P., Heath E.C.;
RT "The relationship between rat major acute phase protein and the
RT kininogens";
RL J. Biol. Chem. 260:12065-12071(1985).
RN [3]
RP SEQUENCE OF 7-430 FROM N.A.
RX MEDLINE-85127561; PubMed-2578992;
RA Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;
RT "Major acute phase alpha 1-protein of the rat is homologous to bovine
RT kininogen and contains the sequence for bradykinin: its synthesis is
RT regulated at the mRNA level.";
RL FEBS Lett. 182:57-61(1985).
RN [4]
RP SEQUENCE OF 1-65 FROM N.A.
RX MEDLINE-87250580; PubMed-2439509;
RA Fung W.-P., Schreiber G.;
RT "Structure and expression of the genes for major acute phase alpha 1-
RT protein (thiostatin) and kininogen in the rat.";
RL J. Biol. Chem. 262:9298-9308(1987).
CC -1- FUNCTION: KININOGENS ARE PLASMA GLYCOPROTEINS WITH A NUMBER OF
CC FUNCTIONS: (1) AS PRECURSOR OF THE ACTIVE PEPTIDE BRADYKININ THEY
CC EFFECT SMOOTH MUSCLE CONTRACTION, INDUCTION OF HYPOTENSION AND
CC INCREASE OF VASCULAR PERMEABILITY. (2) THEY PLAY A ROLE IN BLOOD
CC COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND
CC FACTOR XI NEXT TO FACTOR XII. (3) THEY ARE INHIBITOR OF THIO
CC PROTEASES.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININOGEN
CC II SYNTHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF
CC T-KININOGEN I IS RAISED.
CC -1- PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT
CC IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
CC KALLIKREIN.
CC -1- MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL
CC HMW AND LMW KININOGENS PRODUCED BY ALTERNATIVE SPLICING OF THE
CC SAME GENE, AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I AND T-II.
CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
CC -1- CAUTION: IN ADDITION TO THE CONFLICTS DESCRIBED IN THE FEATURE
CC TABLE, REF.2. SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS: 257,
CC 262,268,269,295,314,315,331,332, AND 389. IN ALL THOSE POSITIONS
CC THE ALTERNATE AMINO-ACID IS THE ONE PRESENT IN T-II KININOGEN.
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CC or send an email to license@isb-sib.ch).
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CC EMBL; M11883; AAA41489.1; -.
CC EMBL; M11661; AAA41570.1; -.
CC EMBL; M16454; AAA41568.1; -.
CC EMBL; X02299; CAA26162.1; ALT_SEQ.
CC PIR; A01286; KGRRT1.
CC PIR; A01285; KGRRTM.
CC PIR; A23897; A23897.
CC PIR; A27115; A27115.
CC GlycoSuiteDB; F01048; -.
CC InterPro; IPR000010; Cystatin.
CC Pfam; PF00031; cystatin; 3.
CC SMART; SM00043; CY; 3.
CC PROSITE; PS00287; CYSTATIN; 2.
CC Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;
CC Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
KW SIGNAL 1 18
FT
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FT CHAIN 19 430 KININOGEN, T-I.
FT CHAIN 19 375 HEAVY CHAIN.
FT PEPTIDE 376 386 T-KININ.
FT CHAIN 387 430 LIGHT CHAIN.
FT DOMAIN 19 135 CYSSTATIN-LIKE 1.
FT DOMAIN 136 257 CYSSTATIN-LIKE 2.
FT DOMAIN 258 375 CYSSTATIN-LIKE 3.
FT DISULFID 28 404 INTERCHAIN (BY SIMILARITY).
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 107 125 BY SIMILARITY.
FT DISULFID 141 144 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 228 247 BY SIMILARITY.
FT DISULFID 263 266 BY SIMILARITY.
FT DISULFID 327 339 BY SIMILARITY.
FT DISULFID 350 369 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 26 28 LNC -> MDR (IN REF. 2).
FT CONFLICT 55 55 V -> L (IN REF. 2).
FT CONFLICT 61 61 E -> K (IN REF. 1).
FT CONFLICT 83 83 C -> Y (IN REF. 3).
FT CONFLICT 166 166 S -> F (IN REF. 2 AND 3).
FT CONFLICT 179 181 REV -> TKI (IN REF. 2).
FT CONFLICT 193 193 N -> D (IN REF. 2).
FT CONFLICT 212 212 S -> F (IN REF. 2).
FT CONFLICT 214 214 R -> H (IN REF. 3).
FT CONFLICT 229 229 T -> R (IN REF. 2).
FT CONFLICT 233 233 H -> Y (IN REF. 2).
FT CONFLICT 257 257 E -> S (IN REF. 2).
FT CONFLICT 262 262 N -> K (IN REF. 2).
FT CONFLICT 264 264 R -> F (IN REF. 2).
FT CONFLICT 268 269 RE -> KN (IN REF. 2).
FT CONFLICT 295 295 I -> L (IN REF. 2).
FT CONFLICT 314 315 VI -> TK (IN REF. 2).
FT CONFLICT 331 332 SK -> TN (IN REF. 2).
FT CONFLICT 389 389 R -> Q (IN REF. 2).
FT CONFLICT 414 414 R -> G (IN REF. 2 AND 3).
FT CONFLICT 415 415 A -> L (IN REF. 2).
FT CONFLICT 420 421 DH -> ER (IN REF. 3).
FT CONFLICT 430 430 P -> S (IN REF. 1).
SQ SEQUENCE 430 AA; 47715 MW; FAEBB78FAF4723C3 CRC64;

Query Match 66.7%; Score 56; DB 1; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.045;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 NNATFYFKIDNVKKA 15
Db 292 HNHIFYFKIDTVKKA 306
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: | | | | | | | | | |

RESULT 6
KNT2_RAT STANDARD; PRT; 430 AA.
AC P08932;
AT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
DE (Thio)statin [Contains: T-kinin].
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86008264; PubMed=2413018;
RX Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT "Primary structures of the mRNAs encoding the rat precursors for

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bradykinin and T-kinin. Structural relationship of kininogens with
major acute phase protein and alpha 1-cysteine proteinase
inhibitor."
J. Biol. Chem. 260:12054-12059(1985).
-|- FUNCTION: KININOGENS ARE PLASMA GLYCOPROTEINS WITH A NUMBER OF
FUNCTIONS: (1) AS PRECURSOR OF THE ACTIVE PEPTIDE BRADYKININ THEY
EFFECT SMOOTH MUSCLE CONTRACTION, INDUCTION OF HYPOTENSION AND
INCREASE OF VASCULAR PERMEABILITY. (2) THEY PLAY A ROLE IN BLOOD
COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND
FACTOR XI NEXT TO FACTOR XII. (3) THEY ARE INHIBITOR OF THIOLE
PROTEASES.
-|- SUBCELLULAR LOCATION: Extracellular.
-|- TISSUE SPECIFICITY: PLASMA.
-|- INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININOGEN
II SYNTHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF
T-KININOGEN I IS RAISED.
-|- PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT
IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
KALLIKREIN.
-|- MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL
HMW AND LMW KININOGENS PRODUCED BY ALTERNATIVE SPLICING OF THE
SAME GENE, AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I AND T-II.
-|- SIMILARITY: CONTAINS 3 CYSSTATIN-LIKE DOMAINS.
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EMBL; M11885; AAA41491.1; -
PIR; B28055; B28055.
GlycoSuiteDB; P08932; -
InterPro; IPR000010; Cystatin.
Pfam; PF00031; cystatin; 3.
SMART; SM00043; Cy; 3.
PROSITE; PS00287; CYSSTATIN; 2.
Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;
Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 430 KININOGEN, T-II.
FT CHAIN 19 375 HEAVY CHAIN.
FT PEPTIDE 376 386 T-KININ.
FT CHAIN 387 430 LIGHT CHAIN.
FT DOMAIN 19 135 CYSSTATIN-LIKE 1.
FT DOMAIN 136 257 CYSSTATIN-LIKE 2.
FT DOMAIN 258 375 CYSSTATIN-LIKE 3.
FT DISULFID 28 404 INTERCHAIN (BY SIMILARITY).
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 107 125 BY SIMILARITY.
FT DISULFID 141 144 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 228 247 BY SIMILARITY.
FT DISULFID 263 266 BY SIMILARITY.
FT DISULFID 327 339 BY SIMILARITY.
FT DISULFID 350 369 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 430 AA; 47524 MW; 43EDF02D1BF55076 CRC64;

Query Match 66.7%; Score 56; DB 1; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.045;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 NNATFYFKIDNVKKA 15
Db 292 HNHIFYFKIDTVKKA 306
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RESULT 7

KNL_BOVIN KNL_BOVIN STANDARD; PRT; 436 AA.
 AC P01046;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Kininogen, LMW I precursor (Thiol proteinase inhibitor) [Contains:
 Bradykinin].
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83117859; PubMed=6572010;
 RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
 RT "Primary structures of bovine liver low molecular weight kininogen
 precursors and their two mRNAs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
 RN [2]
 RP SEQUENCE OF 19-378.
 RX MEDLINE=87137530; PubMed=3546295;
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
 RA Miyata T., Iwanaga S.;
 RT "Bovine high molecular weight kininogen. The amino acid sequence,
 positions of carbohydrate chains and disulfide bridges in the heavy
 chain portion.";
 RL J. Biol. Chem. 262:2768-2779(1987).
 CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
 CC LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
 CC ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LMW-KININOGEN SHOWS
 CC A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH
 CC MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)
 CC NATRIURESIS AND DIURESIS (KIDNEY).
 CC SUBCELLULAR LOCATION: Extracellular.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; LMW I (shown here) and HMW I
 CC (AC P01044); are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
 CC -1- MISCELLANEOUS: LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
 CC INVOLVED IN BLOOD CLOTTING.
 CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; V00426; CAA23709.1; -
 DR PIR; A01283; KGBOLL.
 DR InterPro; IPR000010; Cystatin.
 DR Pfam; PF00031; cystatin; 3.
 DR SMART; SM00043; CV; 3.
 DR PROSITE; PS00287; CYSTATIN; 2.
 KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
 KW Thiol protease inhibitor; Bradykinin; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 436 KININOGEN, LMW I.
 FT CHAIN 19 378 HEAVY CHAIN.
 FT PEPTIDE 380 388 BRADYKININ.
 FT CHAIN 389 436 LIGHT CHAIN.
 FT DOMAIN 19 135 CYSTATIN-LIKE 1.
 FT DOMAIN 136 257 CYSTATIN-LIKE 2.
 FT DOMAIN 258 378 CYSTATIN-LIKE 3.
 FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC...).
 FT CARBOHYD 136 136 O-LINKED (PARTIAL).

FT CARBOHYD 168 168 N-LINKED (GLCNAC...); OR 169.
 FT CARBOHYD 197 197 N-LINKED (GLCNAC...) (PARTIAL).
 FT CARBOHYD 204 204 N-LINKED (GLCNAC...).
 FT DISULFID 27 406 INTERCHAIN.
 FT DISULFID 82 93
 FT DISULFID 106 125
 FT DISULFID 141 144
 FT DISULFID 205 217
 FT DISULFID 228 247
 FT DISULFID 263 266
 FT DISULFID 327 339
 FT DISULFID 350 369
 FT CONFLICT 295 295
 SQ SEQUENCE 436 AA; 48427 MW; F01F7EB6814BCE6C CRC64;
 Query Match 64.3%; Score 54; DB 1; Length 436;
 Best Local Similarity 66.7%; Pred. No. 0.099;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 NNATFYFKIDNVKKA 15
 DB 292 HDGAFYFKIDTVKKA 306
 :: ||||| |||||
 RESULT 8
 KNL_BOVIN KNL_BOVIN STANDARD; PRT; 621 AA.
 AC P01044;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Kininogen, HMW I precursor (Thiol proteinase inhibitor) [Contains:
 Bradykinin].
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84014106; PubMed=6571699;
 RA Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
 RT "A single gene for bovine high molecular weight and low molecular
 weight kininogens.";
 RL Nature 305:545-549(1983).
 RN [2]
 RP SEQUENCE OF 19-378.
 RX MEDLINE=87137530; PubMed=3546295;
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
 RA Miyata T., Iwanaga S.;
 RT "Bovine high molecular weight kininogen. The amino acid sequence,
 positions of carbohydrate chains and disulfide bridges in the heavy
 chain portion.";
 RL J. Biol. Chem. 262:2768-2779(1987).
 RN [3]
 RP SEQUENCE OF 378-393.
 RX MEDLINE=70180420; PubMed=4986212;
 RA Kato H., Nagasawa S., Suzuki T.;
 RT "Studies on the structure of bovine kininogen: cleavages of disulfide
 bonds and of methionyl bonds in kininogen-II.";
 RL J. Biochem. 77:55-68(1975).
 RN [4]
 RP SEQUENCE OF 458-498.
 RX MEDLINE=75170265; PubMed=1169237;
 RA Han Y.N., Komiyama M., Iwanaga S., Suzuki T.;
 RT "Studies on the primary structure of bovine high-molecular-weight
 kininogen. Amino acid sequence of a fragment ('histidine-rich
 peptide') released by plasma kallikrein.";
 RL J. Biochem. 77:55-68(1975).
 CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
 CC HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
 CC HELPING TO POSITION OPTIMALLY PRERALLIKREIN AND FACTOR XI NEXT
 CC TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND

CC PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE
 CC PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS
 CC A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
 CC MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
 CC NUTRIENTS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
 CC (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
 CC IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
 CC RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
 CC (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
 CC ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
 CC ACTION).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; HMW I (shown here) and LMW I
 CC (AC P01046); are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
 CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
 CC -----
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 CC -----

DR EMBL; V01491; CAA24735.1; -.
 DR PIR; A01281; KGB0H1.
 DR PIR; A29559; A29559.
 DR InterPro: IPR000010; Cystatin.
 DR InterPro: IPR002395; Kininogen.
 DR Pfam; PF00031; cystatin; 3.
 DR PRINTS; PR00334; KININOGEN.
 DR SMART; SM00043; CY; 3.
 DR PROSITE; PS00287; CYSTATIN; 2.
 KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
 KW Thiol protease inhibitor; Bradykinin; Blood coagulation;
 KW Inflammatory response; Signal.
 FT SIGNAL 1 18 PROBABLE.
 FT CHAIN 19 621 KININOGEN, HMW I.
 FT CHAIN 19 378 HEAVY CHAIN.
 FT PEPTIDE 380 388 BRADYKININ.
 FT CHAIN 389 621 LIGHT CHAIN.
 FT DOMAIN 19 135 CYSTATIN-LIKE 1.
 FT DOMAIN 136 257 CYSTATIN-LIKE 2.
 FT DOMAIN 258 378 CYSTATIN-LIKE 3.
 FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 136 136 O-LINKED (PARTIAL).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .); OR 169.
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (PARTIAL).
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .).
 FT DISULFID 27 591 INTERCHAIN.
 FT DISULFID 82 93
 FT DISULFID 106 125
 FT DISULFID 141 144
 FT DISULFID 205 217
 FT DISULFID 228 247
 FT DISULFID 263 266
 FT DISULFID 327 339
 FT DISULFID 350 369
 SQ SEQUENCE 621 AA; 68890 MW; D16850BEFE3C55CD CRC64;

Query Match 64.3%; Score 54; DB 1; Length 621;
 Best Local Similarity 66.7%; Pred. No. 0.14;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDNVKKA 15
 Db 292 HDGAFYFKIDTVKKA 306
 :: ||||| |||||

RESULT 9

KNG_MOUSE
 ID KNG_MOUSE STANDARD; PRT; 661 AA.
 AC 008677; 008676;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kininogen precursor [Contains: Bradykinin].
 GN KNG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC STRAIN=CS7BL/6 X CBA; TISSUE=Liver;
 RA Takano M., Kondoh J., Yayama K., Okamoto H.;
 RT "Molecular cloning of cDNAs for mouse low- and high- molecular
 RT kininogen.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
 CC HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
 CC HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
 CC FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
 CC INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
 CC BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF
 CC PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
 CC CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NUTRIENTS AND
 CC DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
 CC MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
 CC PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
 CC OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
 CC A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
 CC INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5)
 CC LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-
 CC KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
 CC CLOTTING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
 CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
 CC -----
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 CC -----

EMBL; D84435; BAA19743.1; -.
 EMBL; D84415; BAA19742.1; -.
 DR MGD; MGI:1097705; Kng
 DR InterPro: IPR000010; Cystatin.
 DR InterPro: IPR002395; Kininogen.
 DR Pfam; PF00031; cystatin; 3.
 DR PRINTS; PR00334; KININOGEN.
 DR SMART; SM00043; CY; 3.
 DR PROSITE; PS00287; CYSTATIN; 1.
 KW Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
 KW Bradykinin; Blood coagulation; Inflammatory response; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 661 KININOGEN.
 FT CHAIN 19 379 KININOGEN HEAVY CHAIN.
 FT CHAIN 380 388 BRADYKININ.
 FT CHAIN 389 661 KININOGEN LIGHT CHAIN.
 FT DOMAIN 19 135 CYSTATIN-LIKE 1.
 FT DOMAIN 136 257 CYSTATIN-LIKE 2.
 FT DOMAIN 258 379 CYSTATIN-LIKE 3.
 FT DOMAIN 439 524 HIS-RICH.
 FT DISULFID 28 631 INTERCHAIN (BY SIMILARITY).


```
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 107 125 BY SIMILARITY.
FT DISULFID 141 144 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 228 247 BY SIMILARITY.
FT DISULFID 263 266 BY SIMILARITY.
FT DISULFID 327 339 BY SIMILARITY.
FT DISULFID 350 369 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 401 432 VSPYIARQGEERDATEQPTGHGWLHEKQ -> RLRA
FT CRYKGLSLKAGAEPAPEQAESSQVKO (IN ISOFORM
FT LMW).
FT VARSPLIC 433 661 MISSING (IN ISOFORM LMW).
SQ SEQUENCE 661 AA; 774460258D58796E CRC64;

Query Match 63.1%; Score 53; DB 1; Length 661;
Best Local Similarity 66.7%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKA 15
I: |||||
Db 292 NDHPFFYKIDTVKKA 306

RESULT 10
LEUD_BUCDN STANDARD; PRT; 208 AA.
AC 085073;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
DE (Isopropylmalate isomerase) (IPMI).
GN LEUD.
OS Buchnera aphidicola (subsp. Diuraphis noxia).
OG Plasmid pLeu-Dn (pBdn1).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118101;
RN [1]
RP SEQUENCE FROM N.A.
RA Baumann L., Baumann P., Moran M.A., Sandstrom J., Thao M.L.;
RT "Genetic characterization of plasmids containing genes encoding
RT enzymes of leucine biosynthesis in endosymbionts (Buchnera) of two
RT related aphid species."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE -> 2-ISOPROPYLMALATE +
CC H(2)O (ALSO CATALYSES 2-ISOPROPYLMALATE + H(2)O -> 3-HYDROXY-
CC 4-METHYL-3-CARBOXY-PENTANONE).
CC -1- SUBUNIT: Leucine biosynthesis; second step.
CC -1- SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUD AND LEUD.
CC
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CC
DR EMBL; AF041837; AAD12603.1; -
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR004431; Leud.
DR Pfam; PF00694; Aconitase_C; 1.
DR TIGRfams; TIGR00171; leud; 1.
KW Leucine biosynthesis; Lyase; Plasmid.
SQ SEQUENCE 208 AA; 24266 MW; E40CD8A63F0396B5 CRC64;

Query Match 48.8%; Score 41; DB 1; Length 208;
Best Local Similarity 42.9%; Pred. No. 7.1;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNATFFFKID 10
I: |||||
Db 63 NKATFFFKID 72

RESULT 12
YS76_CAEEL STANDARD; PRT; 237 AA.
AC Q09619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
```

```
QY 1 NNATFFFKIDNVK 14
I: |||||
Db 155 NQKTFEKLDEFR 168

RESULT 11
NUC2_NEUCR STANDARD; PRT; 1066 AA.
AC Q01317;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ankyrin repeat protein nuc-2.
GN NUC-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-IVA;
RA Peleg Y., Aramayo R., Kang S., Hall J., Metzberg R.;
RT "NUC-2, a component of the phosphate regulated signal transduction
RT pathway in Neurospora crassa, is an ankyrin repeat protein."
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONTROLS PHOSPHORUS ACQUISITION.
CC -1- SIMILARITY: CONTAINS 7 ANK REPEATS.
CC
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CC
DR EMBL; U51118; AAB03277.1; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR004129; GDDP.
DR InterPro; IPR004331; SPX.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF03009; GDDP; 1.
DR Pfam; PF03105; SPX; 1.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT REPEAT 268 298 ANK 1.
FT REPEAT 336 366 ANK 2.
FT REPEAT 370 399 ANK 3.
FT REPEAT 403 432 ANK 4.
FT REPEAT 435 465 ANK 5.
FT REPEAT 470 499 ANK 6.
FT REPEAT 503 532 ANK 7.
SQ SEQUENCE 1066 AA; 117142 MW; 7F672727AFFE92F5 CRC64;

Query Match 48.8%; Score 41; DB 1; Length 1066;
Best Local Similarity 70.0%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFFKID 10
I: |||||
Db 63 NKATFFFKID 72

RESULT 12
YS76_CAEEL STANDARD; PRT; 237 AA.
AC Q09619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
```

DE Hypothetical 27.3 kDa protein ZK892.6 in chromosome III.
GN ZK892.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Lloyd C.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; Z48638; CAA98568.1; -
DR WormPep; ZK892.6; CE01728.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 32703 MW; 3C54CD6CF38EA269 CRC64;

Query Match 46.4%; Score 39; DB 1; Length 237;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 NNATYFKIDN 11
I: ||||| I: I:
DB 60 NDCGTFYKLKLS 70

RESULT 13
YDS4 SCHPO
ID YDS4 SCHPO STANDARD; PRT; 306 AA.
AC O14180;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C4F8.04 in chromosome I.
GN SPAC4F8.04
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gents S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Bozyl K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daya R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovsky G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC -|- SIMILARITY: BELONGS TO THE IMP4 FAMILY.
CC -----
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CC -----
DR EMBL; Z98530; CAB11051.1; -
DR InterPro; IPR002799; Imp4.
DR Pfam; PF01945; Imp4; 1.
KW Hypothetical protein.
SQ SEQUENCE 306 AA; 35835 MW; 2029FBB2358EC01E CRC64;

Query Match 46.4%; Score 39; DB 1; Length 306;
Best Local Similarity 37.5%; Pred. No. 23;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 NNATYFKIDNVKKAR 16
I: ||||| I: I:
DB 168 NGPSFVFTLSNLQTA 183

RESULT 14
HFLK_BUCAI
ID HFLK_BUCAI STANDARD; PRT; 406 AA.
AC P57631;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HflK protein.
GN HFLK OR BU568.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -|- FUNCTION: HFLK AND HFLK COULD ENCODE OR REGULATE A PROTEASE (BY
CC SIMILARITY).
CC -|- SUBUNIT: HFLC AND HFLK MAY INTERACT TO FORM A MULTIMERIC COMPLEX
CC (BY SIMILARITY).
CC -----
CC -|- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY. HFLK SUBFAMILY.
CC -----
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CC -----
DR EMBL; AP001119; BAB13258.1; -
DR InterPro; IPR001107; Band7.
DR Pfam; PF01145; Band.7; 1.
DR PRINTS; PR00721; STOMATIN.
DR SMART; SM00244; PHB; 1.
KW Transmembrane; Complete proteome.
FT TRANSMEM 67
POTENTIAL.

SQ SEQUENCE 406 AA; 45928 MW; 70BA5DD72E537DB2 CRC64;

Query Match 46.4%; Score 39; DB 1; Length 406;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 NNATFYFKIDN 11
|| | : | : ||
Db 334 NNPMEFFSLDN 344

RESULT 15

KCY_UREPA
ID_KCY_UREPA STANDARD; PRT; 224 AA.
AC Q9PQ9;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Cytidylylate kinase (EC 2.7.4.14) (CK) (Cytidine monophosphate kinase)
DE (CMP Kinase).
GN CMK OR UU342.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
RL Nature 407:757-762(2000).
CC -1- CATALYTIC ACTIVITY: ATP + (d)CMP = ADP + (d)CDP.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CYTIDYLATE KINASE FAMILY. SUBFAMILY 1.
CC -----
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CC -----
CC EMBL; AE002131; AAF30751.1; -
DR HSP; P23863; 1CKE.
DR InterPro: IPR003136; Cytidylylate_kin.
DR Pfam: PF02224; Cytidylylate_kin; 1.
DR TIGRfams: TIGR00017; cmk; 1.
KW Transferase; Kinase; ATP-binding; Complete proteome.
FT NP_BIND 11 19 ATP (BY SIMILARITY).
SQ SEQUENCE 224 AA; 25618 MW; AEEF7DF423DADF CRC64;

Query Match 45.2%; Score 38; DB 1; Length 224;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 NATFYFKIDNVK 13
|| | | | | | |
Db 66 NANFENGDNVK 77

Search completed: March 13, 2003, 19:13:26
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:27 ; Search time 33.3333 Seconds
(without alignments)
98.903 Million cell updates/sec

Title: US-09-461-061A-10

Perfect score: 84
Sequence: 1 NNATFFKIDNVKKAR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mnc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	66.7	423	11 P70517	P70517 rattus norv
2	56	66.7	430	11 Q63581	Q63581 rattus norv
3	53	63.1	432	11 Q91XK5	Q91XK5 mus musculu
4	45	53.6	806	5 Q872A3	Q872A3 dictyosteli
5	44	52.4	867	2 Q9KIB1	Q9KIB1 porphyromon
6	43	51.2	466	16 Q8Y807	Q8Y807 listeria mo
7	42	50.0	229	8 Q8WL12	Q8WL12 chlorogonlu
8	42	50.0	244	8 Q8WL11	Q8WL11 ankistrodes
9	42	50.0	657	10 Q9ZUT5	Q9ZUT5 arabidopsis
10	41.5	49.4	469	17 Q29037	Q29037 archaeglob
11	41.5	49.4	1548	5 Q95PI0	Q95PI0 dictyosteli
12	41	48.8	154	16 Q8XMH6	Q8XMH6 clostridium
13	41	48.8	417	16 Q8RH68	Q8RH68 fusobacteri
14	41	48.8	454	17 Q9V0Z1	Q9V0Z1 pyrococcus
15	41	48.8	543	10 Q94IR2	Q94IR2 phaseolus v
16	41	48.8	872	12 Q9EMR4	Q9EMR4 amsacta moo

17	41	48.8	996	10 Q9SGP2	Q9SGP2 arabidopsis
18	41	48.8	1001	5 O17098	O17098 caenorhabdi
19	41	48.8	1346	5 O45699	O45699 caenorhabdi
20	41	48.8	1560	5 Q9GRX5	Q9GRX5 dictyosteli
21	41	48.8	1561	5 Q9U987	Q9U987 dictyosteli
22	40.5	48.2	346	16 Q97KJ4	Q97KJ4 clostridium
23	40	47.6	85	10 Q98RP1	Q98RP1 guillardia
24	40	47.6	179	12 Q86664	Q86664 feline herp
25	40	47.6	202	16 Q8XK08	Q8XK08 clostridium
26	40	47.6	225	16 Q8XN76	Q8XN76 clostridium
27	40	47.6	313	16 Q9PP86	Q9PP86 campylobact
28	40	47.6	333	16 P73616	P73616 synecocyst
29	40	47.6	366	2 Q9X496	Q9X496 mycoplasma
30	40	47.6	388	16 Q97RD7	Q97RD7 streptococc
31	40	47.6	418	17 Q9HJ11	Q9HJ11 thermoplasma
32	40	47.6	431	16 Q9W994	Q9W994 staphylococ
33	40	47.6	532	10 Q8W4P4	Q8W4P4 arabidopsis
34	40	47.6	532	10 Q9SY07	Q9SY07 arabidopsis
35	40	47.6	1014	2 Q8RN21	Q8RN21 campylobact
36	40	47.6	1014	2 Q8RIY7	Q8RIY7 campylobact
37	40	47.6	1021	16 Q8X851	Q8X851 escherichia
38	40	47.6	1191	5 Q9VJN7	Q9VJN7 drosophila
39	40	47.6	1255	5 Q9NK83	Q9NK83 drosophila
40	40	47.6	1790	10 Q8S1X0	Q8S1X0 oryza sativ
41	40	47.6	2817	16 Q97K42	Q97K42 clostridium
42	39	46.4	72	10 Q98S32	Q98S32 guillardia
43	39	46.4	180	16 Q8X336	Q8X336 escherichia
44	39	46.4	184	16 Q97D98	Q97D98 clostridium
45	39	46.4	236	5 Q965N0	Q965N0 caenorhabdi

ALIGNMENTS

RESULT 1

ID	P70517	PRELIMINARY;	PRT;	423 AA.
AC	P70517;			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Major acute phase alpha-1 protein precursor (Fragment).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Cole T.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85149311; PubMed=2579644;			
RA	Cole T., Inglis A., Nagashima M., Schreiber G.;			
RT	"Major acute phase alpha(1)-protein in the rat: Structure, molecular cloning, and regulation of mRNA levels.";			
RL	Biochem. Biophys. Res. Commun. 126:719-724(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85127561; PubMed=2578992;			
RA	Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.;			
RT	"Major acute phase alpha1-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.";			
RL	FEBS Lett. 182:57-61(1985).			
DR	EMBL; K02814; AAA41569.1; -			
DR	InterPro; IPR00010; Cystatin.			
DR	Pfam; PF00031; cystatin; 3.			
DR	SMART; SM00043; Cy; 3.			
DR	PROSITE; PS00287; CYSTATIN; 2.			
KW	Signal.			
NON_TER	1			
FT	SIGNAL	<1		POTENTIAL.

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FT CHAIN 12 423 POTENTIAL.
FT CHAIN 371 379 POTENTIAL.
SQ SEQUENCE 423 AA; 46905 MW; F9E8BD3198547949 CRC64;

Query Match 66.7%; Score 56; DB 11; Length 423;
Best Local Similarity 73.3%; Pred. No. 0.55;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKA 15
Db 285 HNHIFYFKIDTVKKA 299

RESULT 2
Q63581 PRELIMINARY; PRT; 430 AA.
AC Q63581
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Rat T-kininogen (T-KG).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90034172; PubMed=2806908;
RX Anderson K.P., Croyle M.L., Lingrel J.B.;
RT "Primary structure of a gene encoding rat T-kininogen.";
RL Gene 81:119-128(1989).
DR EMBL; M29090; AAA42251.1; JOINED.
DR EMBL; M29083; AAA42251.1; JOINED.
DR EMBL; M29084; AAA42251.1; JOINED.
DR EMBL; M29091; AAA42251.1; JOINED.
DR EMBL; M29085; AAA42251.1; JOINED.
DR EMBL; M29086; AAA42251.1; JOINED.
DR EMBL; M29087; AAA42251.1; JOINED.
DR EMBL; M29088; AAA42251.1; JOINED.
DR EMBL; M29089; AAA42251.1; JOINED.
DR InterPro; IPR000010; Cystatin.
DR Pfam; PF00031; Cystatin; 3.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
SQ SEQUENCE 430 AA; 47618 MW; 45508DEF4BDC978C CRC64;

Query Match 66.7%; Score 56; DB 11; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.55;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKA 15
Db 292 HNHIFYFKIDTVKKA 306

RESULT 3
Q91XK5 PRELIMINARY; PRT; 432 AA.
AC Q91XK5;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Adult female placenta cDNA, RIKEN full-length enriched library,
DE clone:1600027101, full insert sequence (Kininogen).
GN KNG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=PLACENTA;
RX Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,

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RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toyama T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PLACENTA;
RC MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PLACENTA;
RC MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PLACENTA;
RC MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=PLACENTA;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005547; BAB24115.1; -.
DR EMBL; BC018158; AAH18158.1; -.
DR MGD; MGI:1097705; Kng.
DR InterPro; IPR000010; Cystatin.
DR Pfam; PF00031; cystatin; 3.
DR PROSITE; PS00287; CYSTATIN; UNKNOWN_1.
SQ SEQUENCE 432 AA; 47898 MW; 91854EDA5284A16B CRC64;

Query Match 63.1%; Score 53; DB 11; Length 432;
Best Local Similarity 66.7%; Pred. No. 1.7;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKA 15
Db 292 HNHIFYFKIDTVKKA 306

RESULT 4
Q8T2A3 PRELIMINARY; PRT; 806 AA.
ID Q8T2A3

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AC Q8T2A3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein 96.2 kDa protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL EMBL; AC115678; AAL92605.1; -;
KW Hypothetical protein.
SQ SEQUENCE 806 AA; 96216 MW; 2D9BDB77A5BAD1F6 CRC64;
Query Match 53.6%; Score 45; DB 5; Length 806;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVK 14
DB 146 NNYPFFYTLDETCK 159

RESULT 5
Q9KIB1 PRELIMINARY; PRT; 867 AA.
AC Q9KIB1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical tonB-linked outer membrane receptor PG47.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
OC Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W50;
RA Ross B., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,
RA Hocking D., Webb E.;
RT "P. gingivalis polypeptides and nucleic acids.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W50;
RA Ross B.C.;
RT "Genomic analysis of Porphyromonas gingivalis for vaccine discovery.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237557; AF81415.1; -;
DR InterPro; IPR000531; TonB_BoxC.
DR PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 867 AA; 95231 MW; FAB4842E821C4E8E CRC64;
Query Match 52.4%; Score 44; DB 2; Length 867;
Best Local Similarity 53.3%; Pred. No. 93;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NATFFFKIDNVK 16
DB 816 STTFYFNDVADKR 830

RESULT 6
Q8Y807 PRELIMINARY; PRT; 466 AA.
AC Q8Y807;

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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein lmo1112.
GN LMO1112
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-E / SEROVAR 1/2A;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Esibi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nadziek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591977; CAC99190.1; -;
DR Listidist; LMO01112; -;
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 466 AA; 53666 MW; ED1937AD833536F3 CRC64;
Query Match 51.2%; Score 43; DB 16; Length 466;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYFKIDNVK 14
DB 85 YYYKIDNIQ 94

RESULT 7
Q8WL12 PRELIMINARY; PRT; 229 AA.
AC Q8WL12;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 21, Last sequence update)
DE Chloroplast large-subunit ribosomal RNA (rnl), site-specific DNA
DE endonuclease I-Cell gene.
OS Chlorogonium elongatum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Haematococcaceae; Chlorogonium.
OX NCBI_TaxID=52029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97331047; PubMed=9185572;
RA Turmel M., Otis C., Cote V., Lemieux C.;
RT "Evolutionarily conserved and functionally important residues in the
RL Nucleic Acids Res. 25:2610-2619(1997).
DR EMBL; L42860; AAL34336.1; -;
DR InterPro; IPR001982; Endonuc_LAG/HNH.
DR Pfam; PF00961; LAGLIDADG_1; 1.
KW Chloroplast.
SQ SEQUENCE 229 AA; 26622 MW; 5C7EF3D0DC27521E CRC64;
Query Match 50.0%; Score 42; DB 8; Length 229;
Best Local Similarity 72.7%; Pred. No. 54;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 NNATFFFKIDN 11
Db 126 SNATVFFKIDN 136

RESULT 8
Q8WLL1 PRELIMINARY; PRT; 244 AA.
AC Q8WLL1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-JUN-2002 (TREMBlrel. 20, Last sequence update)
DE Chloroplast large-subunit ribosomal RNA (rrnL), site-specific DNA
DE endonuclease I-AstI gene.
OS Ankirodesmus stipitatus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae;
OC Ankirodesmus.
OX NCBI_TaxID=3109;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97331047; PubMed=9185572;
RA Turnel M., Otis C., Cote V., Lemieux C.;
RT "Evolutionarily conserved and functionally important residues in the
RT I-Ceul homing endonuclease.";
RL Nucleic Acids Res. 25:2610-2619(1997).
DR EMBL; L42984; AAL34330.1;
DR InterPro; IPR001982; Endonuc_LAG/HNH.
DR Pfam; PF00961; LAGLIDADG_1; 1.
KW Chloroplast.
SQ SEQUENCE 244 AA; 28065 MW; BA53E451E11FCCF2 CRC64;

Query Match 50.0%; Score 42; DB 8; Length 244;
Best Local Similarity 72.7%; Pred. No. 57;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFFFKIDN 11
Db 130 SNATVFFIDN 140

RESULT 9
Q9ZUT5 PRELIMINARY; PRT; 657 AA.
AC Q9ZUT5;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE At2g37310 protein.
GN At2g37310.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eissen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA;
RA Lin X.;

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RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005896; AAC98051.1;
DR InterPro; IPR002885; PPR.
DR Pfam; PF01535; PPR; 13.
DR TIGRFAMs; TIGR00756; PPR; 12.
SQ SEQUENCE 657 AA; 73342 MW; 9F76D544896EB872 CRC64;

Query Match 50.0%; Score 42; DB 10; Length 657;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTFYKIDNVKAR 16
Db 175 TTYTKDNIESAR 187

RESULT 10
Q29037 PRELIMINARY; PRT; 469 AA.
AC Q29037;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein AFI231.
GN AFI231.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Gwinn M., Hickey E.K., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE001019; AAB90020.1;
DR TIGR; AF1231;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 469 AA; 51663 MW; 3BDAA6AFB1798B43 CRC64;

Query Match 49.4%; Score 41.5; DB 17; Length 469;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 NATFFKIDNVK 13
Db 335 NATFYLKI-NVK 345

RESULT 11
Q95PI0 PRELIMINARY; PRT; 1548 AA.
AC Q95PI0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Histidine kinase Dhkf.
GN DHKF.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxID=44689;

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RN  SEQUENCE FROM N.A.
RP  STRAIN-AX4;
RA  Anjard C., Loomis W.F.;
RT  "The histidine kinases of Dictyostelium.";
RL  (In) Inouye M., Dutta R. (eds.);
RL  Histidine Kinases in Signal Transduction, pp.1-1, Academic Press,
RN  San Diego (2001).
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN-AX4;
RA  Anjard C., Loomis W.F.;
RL  Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF362368; AAK54087.2; -.
KW  Kinase.
SQ  SEQUENCE 1548 AA; 175972 MW; A65783B3AD984596 CRC64;

Query Match      49.48; Score 41.5; DB 5; Length 1548;
Best Local Similarity 60.08; Pred. No. 4.1e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy  1 NNATFYF-KIDNVKK 14
    ||| ||| |||
Db  5 NNSQFYFHKDKIK 19

RESULT 12
Q8XMH6
ID  Q8XMH6 PRELIMINARY; PRT; 154 AA.
AC  Q8XMH6;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Hypothetical protein CPE0713.
GN  CPE0713.
OS  Clostridium perfringens.
OC  Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC  Clostridiales; Clostridiaceae; Clostridium.
OX  NCBI_TaxID=1502;
[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN-13 / TYPE A;
RC  PubMed-11792842;
RA  Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA  Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT  "Complete genome sequence of Clostridium perfringens, an anaerobic
RT  flesh-eater.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR  EMBL; AP003187; BAB80419.1; -.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 154 AA; 17971 MW; 97C25B68403A4B5B CRC64;

Query Match      48.88; Score 41; DB 16; Length 154;
Best Local Similarity 53.88; Pred. No. 53;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy  4 TFYFKIDNVKKAR 16
    ||| ||| |||
Db  128 TLYFKLDYKKKK 140

RESULT 13
Q8RH68
ID  Q8RH68 PRELIMINARY; PRT; 417 AA.
AC  Q8RH68;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Rod shape-determining protein rodA.
GN  FN0042.
OS  Fusobacterium nucleatum (subsp. nucleatum).
OC  Bacteria; Fusobacteria; Fusobacterium.
OX  NCBI_TaxID=76856;

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[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN-ATCC 25586;
RX  MEDLINE=21886394; PubMed=11889109;
RA  Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA  Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA  Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA  Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA  Fonstein M., Kyrpides N., Overbeek R.;
RT  "Genome sequence and analysis of the oral bacterium Fusobacterium
RT  nucleatum strain ATCC 25586.";
RL  J. Bacteriol. 184:2005-2018(2002).
DR  EMBL; AE010519; AAL94255.1; -.
KW  Complete proteome.
SQ  SEQUENCE 417 AA; 46681 MW; 3A42EB3419394F8C CRC64;

Query Match      48.88; Score 41; DB 16; Length 417;
Best Local Similarity 45.78; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy  2 NATFYFKIDNVKKAR 16
    ||| ||| |||
Db  14 NKTLYKKVNDIKKR 28

RESULT 14
Q9V0Z1
ID  Q9V0Z1 PRELIMINARY; PRT; 454 AA.
AC  Q9V0Z1;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Hypothetical protein PAB1940.
GN  PAB1940.
OS  Pyrococcus abyssi.
OC  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC  Pyrococcus.
OX  NCBI_TaxID=29292;
[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN-ORSAY;
RC  Hellig R.;
RA  "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT  structure and evolution.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ248285; CAB49560.1; -.
DR  InterPro: IPR000357; HEAT_REPEAT.
DR  PROSITE: PS50077; HEAT_REPEAT; 1.
KW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 454 AA; 52171 MW; B44FB5C2C7919936 CRC64;

Query Match      48.88; Score 41; DB 17; Length 454;
Best Local Similarity 57.18; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy  1 NNATFYFKIDNVKK 14
    ||| ||| |||
Db  316 SNATSYIKDDAMK 329

RESULT 15
Q94IR2
ID  Q94IR2 PRELIMINARY; PRT; 543 AA.
AC  Q94IR2;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Carotenoid 9,10-9',10' cleavage dioxygenase.
GN  CCD1.
OS  Phaseolus vulgaris (Kidney bean) (French bean).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.

```

```

OX  NCBI_TaxID=3885;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Schwartz S.H., Qin X., Zeevaert J.A.D.;
RT  "Characterization of a Novel Carotenoid Cleavage Dioxygenase from
RL  plants.";
RL  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY029525; AAK38744.1; -
DR  InterPro; IPR004294; RPE65.
DR  Pfam; PF03055; RPE65; 1.
KW  Dioxygenase.
SQ  SEQUENCE 543 AA; 61100 MW; F22C9883A05325F7 CRC64;
    Query Match      48.8%; Score 41; DB 10; Length 543;
    Best Local Similarity 53.3%; Pred. NO. 1.8e+02;
    Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY  2 NATFYFKIDNVKKAR 16
Db  298 NKTIFSDTKKAR 312

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Search completed: March 13, 2003, 19:13:05
Job time : 36.3333 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:07 ; Search time 21 Seconds
(without alignments)
50.762 Million cell updates/sec

Title: US-09-461-061a-1

Perfect score: 45

Sequence: 1 NNATPYFK 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:**
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:**
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	21	Human kininogen D3
2	45	100.0	10	21	Anti-angiogenic D3
3	45	100.0	16	21	Anti-angiogenic D3
4	45	100.0	16	21	Anti-angiogenic D3
5	45	100.0	32	21	Anti-angiogenic D3
6	45	100.0	117	14	Domaine 3, bradyki
7	45	100.0	122	21	Human kininogen D3
8	45	100.0	123	21	Human high mol.wt.
9	45	100.0	248	22	Novel human diagno
10	45	100.0	369	22	Novel human diagno

11	45	100.0	626	23	ABE78707	Human high molecu
12	45	100.0	644	22	ABG21101	Novel human diagno
13	45	100.0	644	23	ABE78710	Human high molecu
14	39	86.7	26	18	AAW54336	Bradykinin analogo
15	36	80.0	78	22	AAO05080	Human polypeptide
16	34	75.6	42	22	AAO74378	Human colon cancer
17	34	75.6	61	22	AAU86501	Novel human connec
18	34	75.6	319	23	ABE53505	Lactococcus lactis
19	34	75.6	376	21	ABE28404	Staphylococcus hom
20	34	75.6	541	22	ABE52487	Escherichia coli p
21	34	75.6	602	20	AAW93820	Bacillus sp. GUS p
22	34	75.6	602	20	AAW93822	Bacillus sp. GUS p
23	34	75.6	602	20	AAW93825	Bacillus sp. codon
24	34	75.6	602	20	AAW93826	Bacillus sp. GUS p
25	34	75.6	602	21	ABE28402	Staphylococcus bet
26	34	75.6	615	21	ABE28408	Codon-optimised st
27	34	75.6	618	20	AAW93821	Bacillus sp. GUS p
28	33	73.3	71	22	AAW82831	Human immune/haema
29	33	73.3	173	21	AAO44316	Arabidopsis thalia
30	33	73.3	251	21	AAO44315	Arabidopsis thalia
31	33	73.3	259	21	AAO44314	Arabidopsis thalia
32	32	71.1	1191	22	ABE60775	Drosophila melanog
33	31	68.9	67	21	AAO34049	Human secreted pro
34	31	68.9	77	22	AAO84819	Human immune/haema
35	31	68.9	89	21	AAO1238	Human secreted pro
36	31	68.9	121	21	AAO81200	Human mutant cysta
37	31	68.9	128	21	AAO81189	Human mutant cysta
38	31	68.9	149	20	AAO36862	Protein which is s
39	31	68.9	158	23	ABO7106	Human ORFX protein
40	31	68.9	161	22	AAO12364	Human polypeptide
41	31	68.9	178	22	ABO9760	Novel human diagno
42	31	68.9	193	16	AAO71919	Macaque platelet a
43	31	68.9	193	18	AAO26505	Macaque platelet-a
44	31	68.9	193	18	AAO23800	Macaque partial pl
45	31	68.9	193	18	AAO9812	Partial macaque pl

ALIGNMENTS

RESULT 1
AAB37455
ID AAB37455 standard; peptide; 9 AA.
XX
AC AAB37455;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human kininogen D3 peptide fragment.
XX
KW Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
XX
OS Homo sapiens.
XX
PN WO200064945-A1.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-GB01571.
XX
PR 22-APR-1999; 99GB-0009133.
XX
PA (BABR-) BABRAHAM INST.
XX
PI Abrahamson M, Barrett AJ;
XX
DR WPI; 2000-687316/67.
XX
PT Inhibition of mammalian legumain or legumain-related endopeptidase by
cystatin involves interaction with second papain-non-reactive site of
cystatin
XX
PS Disclosure; Fig 4; 45pp; English.

CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell
 CC proliferation.

XX
 XX Sequence 16 AA;
 SQ

Query Match 100.0%; Score 45; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.099; 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFK 8
 |||||

Db 9 NNATFFFK 16

RESULT 4
 AAY95410
 ID AAY95410 standard; Peptide; 16 AA.
 AC AAY95410;
 XX
 XX
 DT 25-SEP-2000 (first entry)
 DE Anti-angiogenic D3 peptide.
 DE
 KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200035407-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28465.
 XX
 PR 16-DEC-1998; 98US-0112427.
 XX
 XX (UTEM) UNIV TEMPLE.
 PA (MCCR/) MCCRAE R K.
 XX
 XX McCrae RK;
 PI
 XX
 DR WPI; 2000-442247/38.
 PS
 XX
 XX Composition for inhibiting angiogenesis and endothelial cell
 XX proliferation, inducing endothelial cell apoptosis and treating cancer,
 XX rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 XX 3 analog

Claim 7; Page 26; 44pp; English.

The present sequence is that of a D3 peptide derived from human
 CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell

CC proliferation.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 45; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.099; 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFK 8
 |||||

Db 1 NNATFFFK 8

RESULT 5
 AAY95408
 ID AAY95408 standard; Peptide; 32 AA.
 AC AAY95408;
 XX
 XX
 DT 25-SEP-2000 (first entry)
 DE Anti-angiogenic D3 peptide.
 DE
 KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO200035407-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28465.
 XX
 PR 16-DEC-1998; 98US-0112427.
 XX
 XX (UTEM) UNIV TEMPLE.
 PA (MCCR/) MCCRAE R K.
 XX
 XX McCrae RK;
 PI
 XX
 DR WPI; 2000-442247/38.
 PS
 XX
 XX Composition for inhibiting angiogenesis and endothelial cell
 XX proliferation, inducing endothelial cell apoptosis and treating cancer,
 XX rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 XX 3 analog

Claim 4; Page 26; 44pp; English.

The present sequence is that of a D3 peptide derived from human
 CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell

QY 1 NNATFFFK 8
 |||||

```

Db      13 NNATFFYFK 20

RESULT 6
AAR33350
ID      AAR33350 standard; protein; 117 AA.
XX
AC      AAR33350;
XX
XX      01-JUL-1993 (first entry)
DT
DE      Domaine 3, bradykinin release activating peptide.
XX
XX      Domain 3; human; kininogen; heavy chain; low molecular weight; plasma;
KW      trypsin; platelet; activation; granule contents; hemostasis; thrombin;
KW      tissue plasminogen activator; thrombosis; inflammatory response;
KW      endothelial cell; von Willebrand factor;
XX
OS      Homo sapiens.
XX
XX      Key                               Location/Qualifiers
FH      Peptide                          1..18
FT      /note= "Leader peptide"
FT      Protein                          19..117
FT      /note= "Mature protein"
XX
PN      WO9303748-A.
XX
XX      04-MAR-1993.
PD
XX      13-AUG-1992; 92WO-US06809.
PF
XX      13-AUG-1991; 91US-0744545.
PR      (UTEM ) UNIV TEMPLE.
PA
PI      Jiang Y, Schmaier AB;
XX      WPI; 1993-093714/11.
XX
XX      Use of trypsin-cleavage fragment of human kininogen - for
PT      increasing vascular bradykinin release, for lowering blood
PT      pressure and treating hypertension
XX
PS      Disclosure; Fig 1; 46pp; English.
XX
CC      The sequence given represents domain 3, amino acids 246-362, of
CC      the human kininogen heavy chain. Domain 3 was isolated from low
CC      molecular weight kininogen, derived from human plasma, by cleavage
CC      with trypsin. Domain 3 peptide inhibits platelet activation causing
CC      a marked decrease in the platelets ability to aggregate and secrete
CC      their granule contents. The granule contents comprise proteins which
CC      participate in hemostasis, thrombosis and the inflammatory response.
CC      Domain 3 also inhibits endothelial cell activation shown by a decrease
CC      in secretion of endothelial cell contents such as tissue plasminogen
CC      activator and von Willebrand factor. Domain 3 functions to inhibit
CC      cell activation by blocking thrombin binding to its target cells, the
CC      peptide is a selective inhibitor of thrombin-induced platelet
CC      activation.
XX
SQ      Sequence 117 AA;

Query Match      100.0%; Score 45; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NNATFFYFK 8
        |||||
Db      30 NNATFFYFK 37

RESULT 7
AAB37447

```

```

ID      AAB37447 standard; protein; 122 AA.
XX
XX      AAB37447;
XX
DT      21-FEB-2001 (first entry)
XX
DE      Human kininogen D3.
XX
KW      Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
XX
OS      Homo sapiens.
XX
XX      WO2000064945-A1.
PN
XX      02-NOV-2000.
PD
XX      20-APR-2000; 2000WO-GB01571.
PF
XX      22-APR-1999; 99GB-0009133.
XX
XX      (BABR-) BABRAHAM INST.
PA
PI      Abrahamson M, Barrett AJ;
XX      WPI; 2000-687316/67.
XX
XX      Inhibition of mammalian legumain or legumain-related endopeptidase by
PT      cystatin involves interaction with second papain-non-reactive site of
PT      cystatin
XX
PS      Disclosure; Fig 4; 45pp; English.
XX
CC      The present invention relates to inhibition of the enzymatic activity of
CC      legumain or a legumain-related endopeptidase by cystatin. The inhibition
CC      involves an interaction between legumain and a papain-non-reactive site
CC      of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
CC      performs a protein-processing function. The present sequence is human
CC      kininogen D3, which was used in the present invention. Kininogen is a
CC      type 3 cystatin.
XX
SQ      Sequence 122 AA;

Query Match      100.0%; Score 45; DB 21; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NNATFFYFK 8
        |||||
Db      35 NNATFFYFK 42

RESULT 8
AAY95426
ID      AAY95426 standard; Peptide; 123 AA.
XX
AC      AAY95426;
XX
XX      25-SEP-2000 (first entry)
DT
DE      Human high mol.wt. kininogen domain 3.
XX
XX      Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
KW      endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW      rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
KW      therapy; human; D3 peptide.
XX
OS      Homo sapiens.
XX
XX      WO2000035407-A2.
PN
XX      22-JUN-2000.
PD
XX      02-DEC-1999; 99WO-US28465.
PF

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XX PR 16-DEC-1998; 98US-0112427.
XX PA (UTEM) UNIV TEMPLE.
XX PA (MCCR/) MCCRAE R K.
XX PI McCrae RK;
XX DR WPI; 2000-442247/38.
XX PT Composition for inhibiting angiogenesis and endothelial cell
XX PT proliferation, inducing endothelial cell apoptosis and treating cancer,
XX PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
XX PT 3 analog
XX PS Disclosure; Page 4; 44pp; English.
XX CC The present sequence is that of domain 3 of human high mol. wt.
XX CC kininogen (HK). The invention provides peptides (see AY95405-24)
XX CC that are analogues of certain sites in the HK domain 3,
XX CC specifically Asn275-Lys282, Cys246-Cys249, Leu331-Tyr338 and
XX CC Tyr299-Ser314. The peptides, in which native Cys residues may be
XX CC replaced by Ala residues, inhibit endothelial cell proliferation
XX CC and may also induce endothelial cell apoptosis. Compositions
XX CC including the peptides are used in claimed methods for inhibiting
XX CC angiogenesis, inhibiting endothelial cell proliferation, and
XX CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
XX CC and ocular disorders characterized by undesired vascularization of
XX CC the retina are treated.
XX SQ Sequence 123 AA;
Query Match 100.0%; Score 45; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNATFYFK 8
Db 41 NNATFYFK 48
RESULT 9
ABG21102
ID ABG21102 standard; Protein; 248 AA.
XX AC ABG21102;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #21093.
XX DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
KW Homo sapiens.
XX OS
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS85289.
XX PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity
XX PS Claim 20; SEQ ID NO 51461; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 248 AA;
Query Match 100.0%; Score 45; DB 22; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNATFYFK 8
Db 90 NNATFYFK 97
RESULT 10
ABG21099
ID ABG21099 standard; Protein; 369 AA.
XX AC ABG21099;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #21090.
XX DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
KW Homo sapiens.
XX OS
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS85286.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess

PT	biodiversity	-
XX		
PS	Claim 20; SEQ ID NO 51458; 103pp; English.	
XX		
XX		
CC	The invention relates to isolated polynucleotide (I) and	
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC	and gene mapping, and in recombinant production of (II). The	
CC	polynucleotides are also used in diagnostics as expressed sequence tags	
CC	for identifying expressed genes. (I) is useful in gene therapy techniques	
CC	to restore normal activity of (II) or to treat disease states involving	
CC	(II). (II) is useful for generating antibodies against it, detecting or	
CC	quantitating a polypeptide in tissue, as molecular weight markers and as	
CC	a food supplement. (II) and its binding partners are useful in medical	
CC	imaging of sites expressing (II). (I) and (II) are useful for treating	
CC	disorders involving aberrant protein expression or biological activity.	
CC	The polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABG00010-ABG30377 represent novel human	
CC	diagnostic amino acid sequences of the invention.	
CC	Note: The sequence data for this patent did not appear in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences .	
XX		
CC	Sequence 369 AA;	
CC		
CC	Query Match 100.0%; Score 45; DB 22; Length 369;	
CC	Best Local Similarity 100.0%; Pred. No. 2.5;	
CC	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 NNATFFYFK 8	
DB	333 NNATFFYFK 340	
RESULT 11		
ABB78707		
ID	ABB78707 standard; Protein; 626 AA.	
AC	ABB78707;	
XX		
XX	18-JUL-2002 (first entry)	
DE		
DE	Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1.	
XX		
KW	Human; kininogen; high molecular weight kininogen; HK; D5 domain;	
KW	D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;	
KW	antiatherosclerotic; vasotropic; vulnerable; tranquiliser; thrombolytic;	
KW	ophthalmological; gynaecological; antiulcer; antidiabetic; antiarthritic;	
KW	antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	384..508	
FT	/label= D5_domain	
XX		
XX	WO200214369-A2.	
PN		
XX	21-FEB-2002.	
XX		
XX	24-JUL-2001; 2001WO-US23185.	
XX		
XX	24-JUL-2000; 2000US-220194P.	
PR		
XX	(ATTE-) ATTENUON LLC.	
XX		
PI	Mazar AP, Juarez JC;	
XX		
XX	WPI; 2002-393611/42.	
XX		

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 XX
 PS Claim 20; SEQ ID No 51460; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome,
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 644 AA;

Query Match 100.0%; Score 45; DB 22; Length 644;

Best Local Similarity 100.0%; Pred. No. 4.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFPK 8

|||||||

Db 293 NNATFFPK 300

RESULT 13

ABB78710

ID ABB78710 standard; Protein; 644 AA.

XX AC ABB78710;

XX 18-JUL-2002 (first entry)

XX Human high molecular weight kininogen (HK) protein.

XX Human; kininogen; high molecular weight kininogen; HK; D5 domain;

XX D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;

XX antiatherosclerotic; vasotropic; vulnary; tranquilliser; thrombolytic;

XX ophthalmological; gynaecological; antiulcer; antidiabetic; antiarthritic;

XX antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..18

XX Peptide

XX /label= signal

XX 19..644

XX Protein

XX /label= mature_human_high_molecular_weight_kininogen

XX Disulfide-bond 28..614

XX Disulfide-bond 83..94

XX Disulfide-bond 107..126

XX Disulfide-bond 142..145

XX Disulfide-bond 206..218

XX Disulfide-bond 229..248

XX Disulfide-bond 264..267

XX Disulfide-bond 328..340

XX Disulfide-bond 351..370

XX Domain

XX 402..526

FT /label= D5_domain

XX WO200214369-A2.

XX 21-FEB-2002.

XX 24-JUL-2001; 2001WO-US23185.

XX 24-JUL-2000; 2000US-220194P.

XX (ATTE-) ATTENUON LLC.

XX Mazar AP, Juarez JC;

XX WPI; 2002-393611/42.

XX Novel human kininogen D5 domain polypeptides useful for treating

XX conditions associated with endothelial cell migration, proliferation,

XX invasion or angiogenesis, e.g. arthritis, macular degeneration, benign

XX hyperplasia

XX Disclosure; Fig 1B-E; 84pp; English.

XX The present invention describes an isolated polypeptide (I) that

XX corresponds to the D5 domain of human kininogen, or biologically active

XX peptide fragment, homologue or functional derivative, and which:

XX (a) inhibits angiogenesis; (b) binds to the D5 binding site on

XX endothelial cells (EC); (c) activates signalling pathways leading to the

XX introduction of apoptosis in EC; and/or (d) inhibits the signalling

XX pathway required for maintenance of EC viability. (I) has cytostatic,

XX antitumour, antiatherosclerotic, vasotropic, vulnary, tranquilliser,

XX thrombolytic, ophthalmological, gynaecological, antiulcer, antidiabetic,

XX antiarthritic, antiangiogenic, antiapoptotic and endocrine activities.

XX An antibody (IX) specific for an epitope of (I) is useful for inhibiting

XX tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide

XX (II) or a dimeric or trimeric fusion polypeptide (III) can be used for

XX inhibiting EC migration, proliferation, invasion, or angiogenesis, or

XX for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical

XX composition (X) comprising (I), (II), or (III), can be used for treating

XX a subject having a disease or condition associated with undesired EC

XX migration, proliferation, invasion or angiogenesis. (I), (II), or (III)

XX can be used for isolating a D5 domain binding molecule from a complex

XX mixture and for isolating or enriching cells expressing D5 domain binding

XX sites from a cell mixture. The present sequence represents the human

XX high molecular weight kininogen (HK) protein, which is given in the

XX exemplification of the present invention.

XX Sequence 644 AA;

XX Query Match 100.0%; Score 45; DB 23; Length 644;

XX Best Local Similarity 100.0%; Pred. No. 4.5;

XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 NNATFFPK 8

|||||||

XX Db 293 NNATFFPK 300

XX RESULT 14

XX AAW54336

XX ID AAW54336 standard; peptide; 26 AA.

XX AC AAW54336;

XX 30-JUL-1998 (first entry)

XX Bradykinin analogous peptide 19.

XX Inhibition; thrombin-induced platelet; prevention; platelet aggregation;

XX ADP-induced activation.

XX Synthetic.

XX

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:57 ; Search time 7.66667 Seconds
(without alignments)
30.702 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	117	1	US-08-193-114B-1
2	45	100.0	117	5	PCR-US92-06809-1
3	39	86.7	26	4	US-08-676-242-15
4	34	75.6	602	4	US-09-149-727-2
5	34	75.6	607	4	US-09-149-727-8
6	34	75.6	618	4	US-09-149-727-4
7	31	68.9	193	1	US-08-483-140-30
8	31	68.9	193	2	US-08-485-938A-36
9	31	68.9	441	1	US-08-470-187-8
10	31	68.9	441	1	US-08-318-905-8
11	31	68.9	441	1	US-08-483-232-8
12	31	68.9	441	1	US-08-483-140-8
13	31	68.9	441	2	US-08-485-938A-8
14	31	68.9	441	2	US-08-910-041-8
15	31	68.9	441	3	US-09-328-474-8
16	31	68.9	441	3	US-09-100-546-8
17	31	68.9	441	4	US-09-010-715-8
18	31	68.9	441	4	US-09-577-758-8
19	31	68.9	444	4	US-08-483-140-28
20	31	68.9	444	2	US-08-485-938A-32
21	31	68.9	902	1	US-08-701-846-2
22	31	68.9	2710	1	US-08-480-604A-6
23	31	68.9	2710	2	US-08-405-496A-6
24	31	68.9	2710	4	US-08-915-136-6
25	31	68.9	2710	4	US-08-957-310-6
26	30	66.7	84	4	US-09-227-357-597
27	30	66.7	572	6	5200183-5

Patent No. 5200183

28	30	66.7	602	3	US-08-446-100-1	Sequence 1, Appl
29	30	66.7	602	3	US-08-446-100-2	Sequence 2, Appl
30	30	66.7	602	3	US-08-446-100-3	Sequence 3, Appl
31	30	66.7	602	3	US-08-446-100-4	Sequence 4, Appl
32	30	66.7	602	3	US-08-446-100-5	Sequence 5, Appl
33	30	66.7	602	3	US-08-446-100-6	Sequence 6, Appl
34	30	66.7	602	3	US-08-446-100-7	Sequence 7, Appl
35	30	66.7	602	3	US-08-446-100-8	Sequence 8, Appl
36	30	66.7	602	3	US-08-446-100-9	Sequence 9, Appl
37	30	66.7	602	3	US-08-446-100-10	Sequence 10, Appl
38	30	66.7	602	3	US-08-446-100-11	Sequence 11, Appl
39	30	66.7	602	3	US-08-446-100-12	Sequence 12, Appl
40	30	66.7	602	3	US-08-446-100-13	Sequence 13, Appl
41	30	66.7	602	3	US-08-446-100-14	Sequence 14, Appl
42	30	66.7	602	3	US-08-446-100-15	Sequence 15, Appl
43	30	66.7	602	3	US-08-446-100-16	Sequence 16, Appl
44	30	66.7	602	3	US-08-446-100-17	Sequence 17, Appl
45	30	66.7	602	3	US-08-446-100-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-193-114B-1
; Sequence 1, Application US/08193114B
; Patent No. 5472945
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Jiang, Yongping
; TITLE OF INVENTION: Modulation of Blood
; TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation
; NUMBER OF INVENTIONS: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavoragna &
; ADDRESSEE: Monaco, P.C.
; STREET: 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,114B
FILING DATE: 9 February 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Application
APPLICATION NUMBER: Serial No. 5472945 07/744,545
FILING DATE: 13 August 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-137 CII
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5472945e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: peptide
TOPOLOGY: linear

US-08-193-114B-1
Query Match 100.0%; Score 45; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||
Db 30 NNATFYFK 37

RESULT 2

PCT-US92-06809-1
; Sequence 1, Application PC/TUS9206809
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Jiang, Yongping
; TITLE OF INVENTION: Modulation of Blood
; TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of the
; ADDRESSEE: Commonwealth System of Higher Education
; STREET: 406 University Services
; STREET: Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06809
; FILING DATE: 19910813
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Application
; APPLICATION NUMBER: Serial No. 744,545
; FILING DATE: 13 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-3549
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US92-06809-1

Query Match 100.0%; Score 45; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||
Db 30 NNATFYFK 37

RESULT 3

US-08-676-242-15
; Sequence 15, Application US/08676242C
; Patent No. 6143719
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of Michigan
; APPLICANT: Schmaier, Alvin H.
; APPLICANT: Hasan, Ahmed A.K.
; TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
; FILE REFERENCE: 8820-2 US
; CURRENT APPLICATION NUMBER: US/08/676.242C
; CURRENT FILING DATE: 2000-07-16

; EARLIER APPLICATION NUMBER: 60/000,096
; EARLIER FILING DATE: 1995-06-09
; EARLIER APPLICATION NUMBER: PCT/US96/09940
; EARLIER FILING DATE: 1996-06-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bradykinin
; OTHER INFORMATION: analog
US-08-676-242-15

Query Match 86.7%; Score 39; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
|||||
Db 1 NATFYFK 7

RESULT 4

US-09-149-727-2
; Sequence 2, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Killian, Andrzej
; APPLICANT: Keese, Paul Konrad
; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 190106.405
; CURRENT APPLICATION NUMBER: US/09/149,727
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: US 60/058,263
; EARLIER FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-149-727-2

Query Match 75.6%; Score 34; DB 4; Length 602;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|||||
Db 288 NNATFYFK 295

RESULT 5

US-09-149-727-8
; Sequence 8, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Killian, Andrzej
; APPLICANT: Keese, Paul Konrad
; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 190106.405
; CURRENT APPLICATION NUMBER: US/09/149,727
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: US 60/058,263
; EARLIER FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0

CLASSIFICATION: 435

TELEPHONE: (312) 474-6300
TELETYPE: (312) 474-0448

TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 36;
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-36

Query Match 68.9%; Score 31; DB 2; Length 193;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
:|:|:|
Db 143 SATYFK 149

RESULT 9
US-08-470-187-8
Sequence 8, Application US/08470187
Patent No. 5532152
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine E.
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470.187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532152and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31672
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-470-187-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
:|:|:|
Db 185 SATYFK 191

RESULT 10
US-08-318-905-8
Sequence 8, Application US/08318905
Patent No. 5641669
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318.905
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/133.803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5641669and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-905-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYFK 8
:|:|:|
Db 185 SATYFK 191

RESULT 11
US-08-483-232-8
Sequence 8, Application US/08483232
Patent No. 5656431
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,232
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 565843land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32689
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-232-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATYFK 8
Db 185 SATYFK 191

RESULT 12
US-08-483-140-8
Sequence 8, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-140-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATYFK 8
Db 185 SATYFK 191

RESULT 13
US-08-485-938A-8
Sequence 8, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-938A-8

Query Match 68.9%; Score 31; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0;

QY 2 NATFYFK 8
DB 185 SATYFK 191

RESULT 14
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-910-041-8

Query Match 68.9%; Score 31; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0;

QY 2 NATFYFK 8
DB 185 SATYFK 191

RESULT 15
US-09-328-474-8
; Sequence 8, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-328-474-8

Query Match 68.9%; Score 31; DB 3; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0;

QY 2 NATFYFK 8
DB 185 SATYFK 191

Search completed: March 13, 2003, 19:14:31
Job time : 8.66667 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:12:07 ; Search time 7 Seconds
(without alignments)
52.677 Million cell updates/sec

Title: US-09-461-061A-1

Perfect score: 45

Sequence: 1 NNATFYFK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	75.6	61	10	US-09-764-847-566
2	32	71.1	1659	10	US-09-801-368-118
3	31	68.9	178	9	US-09-768-235B-6
4	31	68.9	224	10	US-09-815-242-13997
5	31	68.9	441	10	US-09-729-402-8
6	31	68.9	1114	10	US-09-740-046-10
7	30	66.7	82	9	US-09-510-332-158
8	30	66.7	84	9	US-09-983-802-597
9	30	66.7	127	10	US-09-764-853-756
10	30	66.7	103	10	US-09-864-761-35808
11	30	66.7	307	10	US-09-825-882-18
12	30	66.7	308	9	US-09-510-332-99
13	30	66.7	308	9	US-09-510-332-155
14	30	66.7	351	10	US-09-780-053-5
15	30	66.7	452	10	US-09-801-368-336
16	30	66.7	545	9	US-09-738-626-5134
17	30	66.7	574	10	US-09-748-739A-4
18	30	66.7	574	10	US-09-748-739A-6
19	30	66.7	574	10	US-09-748-739A-8

20	30	66.7	574	10	US-09-748-739A-17	Sequence 17, Appl
21	30	66.7	574	10	US-09-748-739A-18	Sequence 18, Appl
22	30	66.7	574	10	US-09-748-739A-19	Sequence 19, Appl
23	30	66.7	574	10	US-09-748-739A-20	Sequence 20, Appl
24	30	66.7	574	10	US-09-748-739A-21	Sequence 21, Appl
25	30	66.7	591	10	US-09-764-853-537	Sequence 537, Appl
26	30	66.7	602	10	US-09-748-739A-2	Sequence 2, Appl
27	30	66.7	808	9	US-10-055-364-38	Sequence 38, Appl
28	30	66.7	1007	9	US-09-843-676-86	Sequence 86, Appl
29	30	66.7	1007	9	US-09-766-253-86	Sequence 86, Appl
30	30	66.7	1007	9	US-09-438-486-86	Sequence 86, Appl
31	30	66.7	1007	9	US-10-053-758-86	Sequence 86, Appl
32	30	66.7	1007	9	US-10-054-295-86	Sequence 86, Appl
33	30	66.7	1031	9	US-09-843-676-2	Sequence 2, Appl
34	30	66.7	1031	9	US-09-766-253-2	Sequence 2, Appl
35	30	66.7	1031	9	US-09-438-486-2	Sequence 2, Appl
36	30	66.7	1031	9	US-10-053-758-2	Sequence 2, Appl
37	30	66.7	1031	9	US-10-054-295-2	Sequence 2, Appl
38	30	66.7	2586	10	US-09-905-129-11	Sequence 11, Appl
39	30	66.7	2586	10	US-09-905-129-14	Sequence 11, Appl
40	30	66.7	2586	10	US-09-991-630-11	Sequence 11, Appl
41	30	66.7	2586	10	US-09-991-630-14	Sequence 14, Appl
42	30	66.7	2587	10	US-09-905-129-16	Sequence 16, Appl
43	30	66.7	2587	10	US-09-991-630-16	Sequence 16, Appl
44	30	66.7	2589	10	US-09-991-630-24	Sequence 24, Appl
45	30	66.7	2828	10	US-09-905-129-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-764-847-566
; Sequence 566, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 566
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-847-566

Query Match 75.6%; Score 34; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYF 7
Db 38 NATFYF 43

RESULT 2
US-09-801-368-118
; Sequence 118, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John

```
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 1659
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-118

Query Match      71.1%; Score 32; DB 10; Length 1659;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NNATFFK 8
DB      335 NNATFFWK 342

RESULT 3
US-09-768-235B-6
; Sequence 6, Application US/09768235B
; Publication No. US20030024003A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Marcus
; APPLICANT: Reindl, Andreas
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Freund, Annette
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Renz, Andreas
; APPLICANT: Duwenig, Elke
; APPLICANT: Cirpus, Petra
; APPLICANT: Lerchl, Jens
; APPLICANT: Reski, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins
; TITLE OF INVENTION: Involved in the regulation of cell division, growth and
; TITLE OF INVENTION: biomass formation in plants
; FILE REFERENCE: 0093/000009
; CURRENT APPLICATION NUMBER: US/09/768,235B
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: PCT/EP00/00675
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 2.1/WordPerfect version 6.1
; SEQ ID NO 6
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-768-235B-6

Query Match      68.9%; Score 31; DB 9; Length 178;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NNATFFK 7
DB      73 NNHTYF 79

RESULT 4
US-09-815-242-13997
; Sequence 13997, Application US/09815242
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; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13997
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13997

Query Match      68.9%; Score 31; DB 10; Length 224;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 NNATFFK 7
DB      28 NNSLEYF 34

RESULT 5
US-09-729-402-8
; Sequence 8, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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RESULT 7

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 597
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-597

Query Match 66.7%; Score 30; DB 9; Length 84;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 60 NATFFF 65

RESULT 9
US-09-764-853-756
; Sequence 756, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJO06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 756
; LENGTH: 127
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-764-853-756
Query Match 66.7%; Score 30; DB 10; Length 127;
Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 66 NNGTLFF 72
RESULT 10
US-09-864-761-35808
; Sequence 35808, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35808
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011307.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 7.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.6
; OTHER INFORMATION: EST_HUMAN_HIT: AW937782.1, EVALU8 7.00e-79
; OTHER INFORMATION: SWISSPROT_HIT: O35136, EVALU8 8.00e-12
US-09-864-761-35808

Query Match 66.7%; Score 30; DB 10; Length 183;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFYF 7
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Db 112 NNCTLYF 118

RESULT 11
US-09-825-882-18
; Sequence 18, Application US/09825882
; Patent No. US20020094551A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0279152/RXT
; CURRENT APPLICATION NUMBER: US/09/825,882
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,532
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/247,014
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-882-18

Query Match 66.7%; Score 30; DB 10; Length 307;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYF 7
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Db 93 NSATFWF 99

RESULT 12
US-09-510-332-99
; Sequence 99, Application US/09510332
; Publication No. US2003002278A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: T2R, a NO. US2003002278A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-0980100S
; CURRENT APPLICATION NUMBER: US/09/510,332
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/393,634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 308
; TYPE: PRT

; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat T2R12 (rGR12)
US-09-510-332-99

Query Match 66.7%; Score 30; DB 9; Length 308;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYF 7
|||
Db 93 NSATFWF 99

RESULT 13
US-09-510-332-155
; Sequence 155, Application US/09510332
; Publication No. US2003002278A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: T2R, a NO. US2003002278A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-0980100S
; CURRENT APPLICATION NUMBER: US/09/510,332
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/393,634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse T2R26 (mGR26)
US-09-510-332-155

Query Match 66.7%; Score 30; DB 9; Length 308;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYF 7
|||
Db 93 NSATFWF 99

RESULT 14
US-09-780-053-5
; Sequence 5, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129 5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 351

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; TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-09-780-053-5
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Query Match          66.7%; Score 30; DB 10; Length 351;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      2 NATFYFK 8
Db      272 NSTFYIK 278
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RESULT 15

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US-09-801-368-336
; Sequence 336, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-336
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Query Match          66.7%; Score 30; DB 10; Length 452;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      1 NNATFYFK 8
Db      406 NNKTFELK 413
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Search completed: March 13, 2003, 19:15:00
Job time : 8 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:37 ; Search time 9 Seconds
(without alignments)
85.453 Million cell updates/sec

Title: US-09-461-061a-1

Perfect score: 45

Sequence: 1 NNATYFK 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	427	1 KGHUL1	Kininogen, LMW pre
2	45	100.0	644	1 KGHUL1	kininogen, LMW pre
3	39	86.7	433	2 A28055	K-kininogen, LMW I
4	39	86.7	639	2 A25486	kininogen, HMW I p
5	36	80.0	858	2 T24062	hypothetical prote
6	36	80.0	1132	2 T31107	telomerase reverse
7	35	77.8	182	2 T24206	hypothetical prote
8	34	75.6	71	2 B83803	hypothetical prote
9	34	75.6	182	2 T06978	ABA-induced plasma
10	34	75.6	273	2 F86924	hypothetical prote
11	34	75.6	319	2 A86650	rhamnosyltransfera
12	34	75.6	440	2 T11319	NADH2 dehydrogenas
13	34	75.6	497	2 G96611	hypothetical cytochrom
14	34	75.6	630	2 T25830	hypothetical prote
15	34	75.6	758	2 T31994	hypothetical prote
16	34	75.6	949	2 H97322	DNA/RNA helicase,
17	33	73.3	303	2 T32658	hypothetical prote
18	33	73.3	332	2 T01483	hypothetical prote
19	33	73.3	459	2 F69403	hypothetical prote
20	33	73.3	603	2 T07849	cholinesterase (EC
21	33	73.3	706	2 D84466	hypothetical prote
22	33	73.3	895	2 T23191	hypothetical prote
23	32	71.1	484	2 A40774	phosphocholine-bin
24	32	71.1	562	2 AF0852	secretory protein
25	32	71.1	563	2 S54420	invasion protein I
26	32	71.1	567	2 E91095	type III secretion
27	32	71.1	567	2 A85941	type III secretion
28	32	71.1	606	2 T10982	NADH2 dehydrogenas
29	32	71.1	1215	2 T25078	hypothetical prote

RESULT 1

KGHUL1

kininogen, LMW precursor [validated] - human

N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen

N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen

C;Species: Homo sapiens (man)

C;Date: 06-Jul-1982 #sequence.revision 27-Nov-1985 #text.change 08-Dec-2000

C;Accession: A01280; B25276; A27900; A27699; A31905; A34030

R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.

Biochemistry 23, 5691-5697, 1984

A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide

A;Reference number: A90490; MUID:85122621; PMID:6441591

A;Accession: A01280

A;Molecule type: mRNA

A;Residues: 1-427 <OHK>

A;Cross-references: GB:K02566; NID:g177889; PIDN:AAA35497.1; PID:g177890

R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.

J. Biol. Chem. 260, 8601-8609, 1985

A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and 1

A;Reference number: A92544; MUID:85234582; PMID:2989293

A;Accession: B25276

A;Molecule type: mRNA

A;Residues: 1-427 <FAK>

A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59551.1; PID:g386853

R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Rauth, G.; Mueller-Esterl, W.

in Kinins IV, part A, Greenbaum, L.M., and Margolius, H.S., eds., pp.91-95, Plenum, N

A;Title: Amino acid sequence of the light chain of human low molecular mass kininogen

A;Reference number: A27900

A;Accession: A27900

A;Molecule type: protein

A;Residues: 390-427 <LOT>

R;Mindrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.

Biochem. Biophys. Res. Commun. 152, 519-526, 1988

A;Title: A new kinin moiety in human plasma kininogens.

A;Reference number: A27699; MUID:88209021; PMID:3365237

A;Accession: A27699

A;Molecule type: protein

A;Residues: 380-389 <MIN>

R;Maeda, H.; Matsumura, Y.; Kato, H.

J. Biol. Chem. 263, 16051-16054, 1988

A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f

A;Reference number: A31905; MUID:89034061; PMID:3182782

A;Accession: A31905

A;Molecule type: protein

A;Residues: 391-389 <MAE>

R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.

Biochem. Biophys. Res. Commun. 150, 511-516, 1988

A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p

A;Reference number: A34030; MUID:88106632; PMID:3337729

A;Accession: A34030

A;Molecule type: protein

A;Residues: 380-389 <SAS>

R:Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 260, 8610-8617, 1985
 A:Title: Structural organization of the human kininogen gene and a model for its evolution
 A:Reference number: A92545; MUID:85234583; PMID:2989294
 A:Contents: annotation; gene organization
 R:Pierce, J.V.
 Fed. Proc. 27, 52-57, 1968
 A:Title: Structural features of plasma kinins and kininogens.
 A:Reference number: A91455; MUID:90255622; PMID:4952632
 A:Contents: annotation; bradykinin
 C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form (see A:91455).
 C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
 C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, 1
 xproline residue is present in the kininogen prior to the release of bradykinin.
 C:Genetics:
 A:Gene: GDB:GNG
 A:Cross-references: GDB:125256; OMIM:228960
 A:Map position: 3q27-3q27
 A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
 C:Superfamily: kininogen; cystatin homology
 C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyco
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-427/Product: LMW prokininogen (kininogen I) #status predicted <MAT>
 F:19-389,390-427/Product: LMW kininogen II #status predicted <MAT2>
 F:19-379/Product: LMW kininogen heavy chain #status predicted <HCH>
 F:19-131/Domain: cystatin homology <CY1>
 F:142-253/Domain: cystatin homology <CY2>
 F:264-375/Domain: cystatin homology <CY3>
 F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KB DY>
 F:381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
 F:390-427/Product: LMW kininogen light chain #status experimental <LCH>
 F:19/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:28-407,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bonds:
 F:48,169,205,294/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
 F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 F:401/Binding site: carboxylate (Thr) (covalent) #status absent

Query Match 100.0% Score 45; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFK 8
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 Db 293 NNATFFK 300

RESULT 2
 KGHUHI
 kininogen, HMW precursor [validated] - human
 N:Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
 N:Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular we
 C:Species: Homo sapiens (man)
 C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000
 C:Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; S02
 Biochemistry 23, 5691-5697, 1984
 A:Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identifi
 A:Reference number: A90490; MUID:85122621; PMID:6441591
 A:Accession: A01279
 A:Molecule type: mRNA
 A:Residues: 1-389 <ORF>
 A:Cross-references: GB:K02566; NID:gl77889
 R:Takagaki, Y.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A:Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
 A:Reference number: A92544; MUID:85234582; PMID:2989293
 A:Accession: A25276
 A:Molecule type: mRNA
 A:Residues: 1-592, '1', 594-644 <TAK>
 A:Cross-references: GB:M11437; NID:q186751; PIDN:AA859550.1; PID:q386852
 R:Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.

FEBS Lett. 321, 93-97, 1993
 A:Title: Cloning, expression and characterization of human kininogen domain 3.
 A:Reference number: S32422; MUID:93223854; PMID:8467916
 A:Accession: S32422
 A:Molecule type: mRNA
 A:Residues: 'ANSM', 253-377 <AUE>
 A:Note: differences are due to known cloning artifacts
 R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A:Title: The amino acid sequence of the light chain of human high-molecular-mass kini
 A:Reference number: A91153; MUID:86030270; PMID:4054110
 A:Accession: A91153
 A:Molecule type: protein
 A:Residues: 379-644 <LOT>
 A:Note: the bradykinin sequence preceding the light chain sequence was not determined
 R:Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
 Eur. J. Biochem. 154, 471-478, 1986
 A:Title: Completion of the primary structure of human high-molecular-mass kininogen.
 A:Reference number: A24871; MUID:86108361; PMID:3484703
 A:Accession: A24871
 A:Molecule type: protein
 A:Residues: 'Z', 20-380 <KEL1>
 R:Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
 In Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New
 A:Title: Amino acid sequence of the light chain of human high molecular mass kininoge
 A:Reference number: A27899
 A:Accession: A27899
 A:Molecule type: protein
 A:Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
 R:Mindeiro, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
 Biochem. Biophys. Res. Commun. 152, 519-526, 1988
 A:Title: A new kinin moiety in human plasma kininogens.
 A:Reference number: A27699; MUID:88209021; PMID:3365237
 A:Accession: A27699
 A:Molecule type: protein
 A:Residues: 380-389 <MIN>
 R:Maeda, H.; Matsumura, Y.; Kato, H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A:Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic f
 A:Reference number: A31905; MUID:89034061; PMID:3182782
 A:Accession: A31905
 A:Molecule type: protein
 A:Residues: 381-389 <MAE>
 R:Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A:Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human p
 A:Reference number: A34030; MUID:88106632; PMID:3337729
 A:Accession: A34030
 A:Molecule type: protein
 A:Residues: 380-389 <SAS>
 R:Lenarcic, B.; Gabrijeleic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A:Title: Human cathepsin B and cysteine proteinase inhibitors (CPis) in inflammatory
 A:Reference number: S02482; MUID:89076517; PMID:3264507
 A:Accession: S02482
 A:Molecule type: protein
 A:Residues: 1-19; 189-192; 310-314; 381-389 <LEN1>
 R:Kato, H.; Matsumura, Y.; Maeda, H.
 FEBS Lett. 232, 252-254, 1988
 A:Title: Isolation and identification of hydroxyproline analogues of bradykinin in hu
 A:Reference number: A61495; MUID:88211869; PMID:3366244
 A:Accession: A61495
 A:Molecule type: protein
 A:Residues: 380-389 <KAT1>
 A:Experimental source: urine
 A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A:Accession: B61495
 A:Molecule type: protein
 A:Residues: 381-389 <KAT2>
 A:Experimental source: urine
 A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A:Accession: C61495
 A:Molecule type: protein

A;Residues: 380-389 <KAT3>
R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A;Reference number: S14303; MUID:91192133; PMID:2013314
A;Accession: S14447
A;Molecule type: protein
A;Residues: 264-359; 'N', 361-375 <LEN2>
R;Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity
A;Reference number: S55239; MUID:95251593; PMID:7733867
A;Accession: S55239
A;Molecule type: protein
A;Residues: 450-452; 'X', 454; 'Y', 456 <LIT>
R;Straczek, J.; Maachi, F.; le Nguyen, D.; Becchi, M.; Heullin, M.H.; Nabet, P.; Belleville, J.
FEBS Lett. 373, 207-211, 1995
A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like growth factor release
A;Reference number: S68059; MUID:96033974; PMID:7589467
A;Accession: S68059
A;Molecule type: protein
A;Residues: 431-434 <STR>
R;Kitamura, N.; Kitagawa, H.; Fukushima, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen gene and a model for its evolution
A;Reference number: A92545; MUID:85234583; PMID:2989294
A;Contents: annotation; gene organization
R;Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A;Title: Structural features of plasma kinins and kininogens.
A;Reference number: A91455; MUID:90255622; PMID:4952632
A;Contents: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the blood coagulation cascade
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is important for biological activity
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, and its release is regulated by the kininogen prior to the release of bradykinin.
C;Genetics:
A;Gene: GDB:KNG
A;Cross-references: GDB:125256; OMIM:228960
A;Map position: 3q27-3q27
A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duplication
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379-390-644/Product: HMW kininogen II #status experimental <MAT2>
F;19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
F;390-644/Domain: HMW kininogen light chain #status experimental <LCH>
F;421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F;431-434/Product: low molecular weight growth promoting factor #status experimental <GH>
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;28-614, 83-94, 107-126, 142-145, 206-218, 229-248, 264-267, 328-340, 351-370/Disulfide bonds:
F;48/Binding site: carboxyhydrate (Asn) (covalent) #status absent
F;169, 205, 294/Binding site: carboxyhydrate (Asn) (covalent) #status experimental
F;379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
F;383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;401, 533, 542, 546, 557, 571, 593, 628/Binding site: carboxyhydrate (Thr) (covalent) #status experimental
F;577/Binding site: carboxyhydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 45; DB 1; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFYFK 8

Db 293 NNATFFYFK 300

RESULT 3

A28055
K-kininogen, LMW I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
C;Accession: A28055
R;Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin a and b
A;Reference number: A92496; MUID:86008264; PMID:2413018
A;Accession: A28055
A;Molecule type: mRNA
A;Residues: 1-433 <FUR>
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-433/Product: K-kininogen, LMW I #status predicted <MAT>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>

Query Match 86.7%; Score 39; DB 2; Length 433;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYFK 8

Db 293 NNATFFYFK 300

RESULT 4

A23486
kininogen, HMW I precursor - rat
N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family
A;Reference number: A92625; MUID:87137443; PMID:3029068
A;Accession: A25486
A;Molecule type: mRNA
A;Residues: 1-639 <KIT>
A;Note: the authors translated the codon CAA for residue 347 as Asn
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-639/Product: kininogen, HMW I #status predicted <MAT>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>

Query Match 86.7%; Score 39; DB 2; Length 639;
Best Local Similarity 87.5%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYFK 8

Db 293 NNATFFYFK 300

RESULT 5

T24062
hypoetical protein R09A8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24062
R;Wilkinson, J.
submitted to the EMBL Data Library, November 1995

A:Reference number: Z19836
A:Accession: T24062
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-858 <WIL>
A:Cross-references: EMBL:Z68009; PIDN:CAA92004.1; GSPDB:GN00028; CESP:R09A8.2
C:Genetics:
A:Gene: CESP:R09A8.2
A:Map position: X
A:Introns: 197/1; 324/3; 377/3; 435/3; 495/3; 587/1; 627/3; 730/3; 812/1

Query Match 80.0%; Score 36; DB 2; Length 858;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
||| :|||
Db 49 NESTFYFK 56

RESULT 6
T31107
telomerase reverse transcriptase - Oxytricha trifallax
C:Species: Oxytricha trifallax
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T31107
R:Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A:Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha
A:Reference number: Z20985; MUID:98337940; PMID:9671703
A:Accession: T31107
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1132 <BRY>
A:Cross-references: EMBL:AF060230; NID:g3342795; PID:g3342796; PIDN:AAC39163.1
C:Genetics:
A:Gene: TERT

Query Match 80.0%; Score 36; DB 2; Length 1132;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
||| :|||
Db 1001 NNISFYFK 1008

RESULT 7
T24206
hypothetical protein R12H7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000
C:Accession: T24206
R:Coles, L.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19854
A:Accession: T24206
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-182 <WIL>
A:Cross-references: EMBL:Z50755; PIDN:CAA90635.1; GSPDB:GN00028; CESP:R12H7.3
C:Genetics:
A:Gene: CESP:R12H7.3
A:Map position: X
A:Introns: 150/3
C:Superfamily: human S-phase kinase-associated protein 1A

Query Match 77.8%; Score 35; DB 2; Length 182;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
||| :|||
Db 161 NNATLFFK 168

RESULT 8
B83803
hypothetical protein BH1226 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B83803
R:Ikami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:gi10173727; PIDN:BA04945.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1226

Query Match 75.6%; Score 34; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYF 7
||| :|||
Db 43 NATFYF 48

RESULT 9
T06978
ABA-induced plasma membrane protein PM 19 - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C:Accession: T06978
R:Koike, M.; Takezawa, D.; Arakawa, K.; Yoshida, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z15842
A:Accession: T06978
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-182 <KOI>
A:Cross-references: EMBL:U80037; NID:gl724111; PIDN:AAB38504.1; PID:gl724112
A:Experimental source: cv. Chihoku
C:Genetics:
A:Note: WTABPM

Query Match 75.6%; Score 34; DB 2; Length 182;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYF 7
||| :|||
Db 47 NGATFYF 53

RESULT 10
F86924
hypothetical protein [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: F86924
R:Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.N.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: F86924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <STO>
A:Cross-references: GB:AL450380; NID:gl13092504; PIDN:CAC29634.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML0126

Query Match 75.6%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 30;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
||| |||
DB 20 NNAQFYF 26

RESULT 11

A:Accession: A86650
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <STO>
A:Cross-references: GB:AE005176; PID:gl2723056; PIDN:AAK04299.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: rpgB

Query Match 75.6%; Score 34; DB 2; Length 319;
Best Local Similarity 85.7%; Pred. No. 35;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
||| |||
DB 80 NNAQFYF 86

RESULT 12

A:Accession: T11319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-440 <TUR>
A:Cross-references: EMBL:AF116775; NID:g4378766; PID:g4378773; PIDN:AAD19671.1
C:Genetics:
A:Gene: nad2
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match 75.6%; Score 34; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 48;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
||| |||

Db 238 NNALFYF 244

RESULT 13

A:Accession: G96611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <STO>
A:Cross-references: GB:AL450380; NID:gl13092504; PIDN:CAC29634.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML0126

Query Match 75.6%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 30;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
||| |||
DB 20 NNAQFYF 26

RESULT 14

A:Accession: T25830
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-630 <SCH>
A:Cross-references: EMBL:U98174; PIDN:AA42276.1; GSPDB:GN00019; CESP:M01A10.4
A:Experimental source: strain Bristol N2; clone M01A10
C:Genetics:
A:Gene: CESP:M01A10.4
A:Map position: 1
A:Introns: 10/2; 249/3; 284/1

Query Match 75.6%; Score 34; DB 2; Length 497;
Best Local Similarity 85.7%; Pred. No. 54;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NATFFYF 8
| |||||
DB 64 NLTFYF 70

RESULT 15

A:Accession: T25830
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-630 <SCH>
A:Cross-references: EMBL:U98174; PIDN:AA42276.1; GSPDB:GN00019; CESP:M01A10.4
A:Experimental source: strain Bristol N2; clone M01A10
C:Genetics:
A:Gene: CESP:M01A10.4
A:Map position: 1
A:Introns: 10/2; 249/3; 284/1

Query Match 75.6%; Score 34; DB 2; Length 630;
Best Local Similarity 75.0%; Pred. No. 68;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 8
||| |||||
DB 444 SNAQFYF 451

RESULT 15

A:Accession: T31994
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <STO>
A:Cross-references: GB:AL450380; NID:gl13092504; PIDN:CAC29634.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML0126

Query Match 75.6%; Score 34; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 48;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
||| |||

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31994
 R:Henkhaus, J.; Wohldmann, P.; Beck, C.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid C49D10.
 A:Reference number: Z21108
 A:Accession: T31994
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-758 <HEN>
 A:Cross-references: EMBL:AF016665; PIDN:AAC71186.1; GSPDB:GN000020; CESP:C49D10.1
 A:Experimental source: strain Bristol N2; clone C49D10
 C:Genetics:
 A:Gene: CESP:C49D10.1
 A:Map position: 2
 A:Introns: 438/2

Query Match 75.6%; Score 34; DB 2; Length 758;
 Best Local Similarity 75.0%; Pred. No. 82;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 :|||
 Db 598 SNAQFYFK 605

Search completed: March 13, 2003, 19:14:01
 Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:02 ; Search time 5 Seconds
(without alignments)
66.362 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATFFFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	644	1	KNG_HUMAN
2	39	86.7	639	1	KNG_RAT
3	36	80.0	1132	1	TERT_OXYTR
4	33	73.3	603	1	CHLE_MOUSE
5	32	71.1	562	1	INVG_SALTY
6	32	71.1	606	1	NU5M_PIG
7	32	71.1	1590	1	GCN2_YEAST
8	31	68.9	82	1	U2AG_PIG
9	31	68.9	196	1	HIS5_BUCAI
10	31	68.9	239	1	U2AG_MOUSE
11	31	68.9	240	1	U2AG_HUMAN
12	31	68.9	264	1	U2AG_DROME
13	31	68.9	334	1	ARGC_ECOLI
14	31	68.9	341	1	OMPU_VIBCH
15	31	68.9	434	1	KNL2_BOVIN
16	31	68.9	441	1	PAFA_HUMAN
17	31	68.9	444	1	PAFA_CANFA
18	31	68.9	619	1	KNH2_BOVIN
19	31	68.9	623	1	RSD1_YEAST
20	31	68.9	901	1	VEF_GVPT
21	31	68.9	901	1	VEF_GVTN
22	31	68.9	902	1	VEF_GVHA
23	31	68.9	988	1	ST23_YEAST
24	31	68.9	1066	1	NUC2_NEUCR
25	31	68.9	2710	1	TOXA_CLODI
26	31	68.9	4725	1	DYHC_DICDI
27	30	66.7	163	1	SFAS_ECOLI
28	30	66.7	196	1	HIS5_METJA
29	30	66.7	208	1	LEUD_BUCDN
30	30	66.7	237	1	YS76_CABEL
31	30	66.7	251	1	X456_MYCPU
32	30	66.7	259	1	KKA6_ACTBA
33	30	66.7	331	1	NIXA_HELPJ

34	30	66.7	331	1	NIXA_HELPY	Q48262 helicobacte
35	30	66.7	365	1	NMPC_ECOLI	P21420 escherichia
36	30	66.7	383	1	CYB_APILI	P34845 apis mellif
37	30	66.7	397	1	YAK7_SCHPO	Q09919 schizosacch
38	30	66.7	452	1	SMP1_YEAST	P38128 saccharomyc
39	30	66.7	477	1	GLGA_STRPN	Q97455 streptococc
40	30	66.7	492	1	CPBU_MOUSE	O55071 mus musculu
41	30	66.7	537	1	YIV9_YEAST	P40583 saccharomyc
42	30	66.7	541	1	UL21_V2VD	P09289 varicella-z
43	30	66.7	581	1	CHLE_RABIT	P21927 oryctolagus
44	30	66.7	602	1	CHLE_HUMAN	P06276 homo sapien
45	30	66.7	603	1	NU5M_MYOGL	O63908 myoxus glis

ALIGNMENTS

RESULT 1
KNG_HUMAN
ID KNG_HUMAN STANDARD; PRT; 644 AA.
AC P01042; P01043;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kininogen precursor (Alpha-2-thiol proteinase inhibitor) [Contains:
DE Bradykinin].
GN KNG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
RC TISSUE=Liver;
RX MEDLINE=85234582; PubMed=2989293;
RA Takagaki Y., Kitamura N., Nakanishi S.;
RT "Cloning and sequence analysis of cDNAs for human high molecular
RT weight and low molecular weight prekininogens. Primary structures of
RT two human prekininogens.";
RL J. Biol. Chem. 260:8601-8609(1985).
RN [2]
RP GENE STRUCTURE.
RX MEDLINE=85234583; PubMed=2989294;
RA Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T.,
RA Nakanishi S.;
RT "Structural organization of the human kininogen gene and a model for
RT its evolution.";
RL J. Biol. Chem. 260:8610-8617(1985).
RN [3]
RP SEQUENCE OF 1-401 FROM N.A.
RX MEDLINE=85122621; PubMed=6441591;
RA Ohkubo I., Kurachi K., Takasawa T., Shiohara H., Sasaki M.;
RT "Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and
RT its identity with low molecular weight kininogen.";
RL Biochemistry 23:5691-5697(1984).
RN [4]
RP SEQUENCE OF 379-644.
RX MEDLINE=86030270; PubMed=4054110;
RA Lottspeich F., Kellermann J., Henschen A., Foertsch B.,
RA Mueller-Esterl W.;
RT "The amino acid sequence of the light chain of human high-molecular-
RT mass kininogen.";
RL Eur. J. Biochem. 152:307-314(1985).
RN [5]
RP SEQUENCE OF 381-389.
RX MEDLINE=90255622; PubMed=4952632;
RA Pierce J.V.;
RT "Structural features of plasma kinins and kininogens.";
RL Fed. Proc. 27:52-57(1968).
RN [6]
RP DISULFIDE BONDS.
RA Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
RT "Disulfide bonds in bovine HMW kininogens.";

RT "Primary structures of the mRNAs encoding the rat precursors for
RT bradykinin and T-kinin. Structural relationship of kininogens with
RT major acute phase protein and alpha 1-cysteine proteinase
RT inhibitor.";
RL J. Biol. Chem. 260:12054-12059(1985).
RN [3]
RP SEQUENCE OF 1-65 FROM N.A.
RC STRAIN=Buffalo;
RA MEDLINE=87250580; PubMed=2439509;
RX Fung W.-P., Schreiber G.;
RT "Structure and expression of the genes for major acute phase alpha 1-
RT protein (thiostatin) and kininogen in the rat.";
RL J. Biol. Chem. 262:9298-9308(1987).
RN [4]
RP SEQUENCE OF 1-41 FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=87137465; PubMed=3818598;
RA Kageyama R., Kitamura N., Ohkubo H., Nakanishi S.;
RT "Differing utilization of homologous transcription initiation sites
RT of rat K and T kininogen genes under inflammation condition.";
RL J. Biol. Chem. 262:2345-2351(1987).
CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOLESTERASES; (2)
CC HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
CC HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
CC INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
CC BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF
CC PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CC CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
CC DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
CC MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
CC PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
CC OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
CC A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
CC INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5)
CC LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-
CC KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
CC CLOTTING.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
CC -1- MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL
CC HMW/LMW KININOGENS AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I AND
CC T-II.
CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
CC
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CC
CC EMBL: L29428; AAA41486.1; -
CC EMBL: M11884; AAA41487.1; -
CC EMBL: M14369; AAA41484.1; -
CC EMBL: M14369; AAA41485.1; ALT_SEQ.
CC EMBL: M16455; AAA41482.1; -
CC PIR: A25486; A25486.
CC PIR: A28055; A28055.
CC InterPro: IPR000010; Cystatin.
CC Pfam: PF00031; cystatin; 3.
CC PRINTS: PR00034; cystatin.
CC SMART: SM00043; CY; 3.
CC PROSITE: PS00287; CYSTATIN; 2.
CC GlycoProtein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
KW Bradykinin; Blood coagulation; Inflammatory response; Signal;
KW Alternative splicing; Multigene family.
FT SIGNAL 1 18

FT CHAIN 19 639 KININOGEN.
FT CHAIN 19 380 KININOGEN HEAVY CHAIN.
FT PEPTIDE 381 389 BRADYKININ.
FT CHAIN 390 639 KININOGEN LIGHT CHAIN.
FT DOMAIN 19 136 CYSTATIN-LIKE 1.
FT DOMAIN 137 258 CYSTATIN-LIKE 2.
FT DOMAIN 259 380 CYSTATIN-LIKE 3.
FT DOMAIN 439 514 HIS-RICH.
FT DISULFID 28 609 INTERCHAIN (BY SIMILARITY).
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 107 126 BY SIMILARITY.
FT DISULFID 142 145 BY SIMILARITY.
FT DISULFID 206 218 BY SIMILARITY.
FT DISULFID 229 248 BY SIMILARITY.
FT DISULFID 264 267 BY SIMILARITY.
FT DISULFID 328 340 BY SIMILARITY.
FT DISULFID 351 370 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 402 433 VSPSYARVQBERDPGNEQCPHGHGHLHAKQ -> RLMS
FT CEYGRLLKAGAPAPERAESTVTP (IN ISOFORM
FT LMW).
FT VARSPLIC 434 639 MISSING (IN ISOFORM LMW).
FT CONFLICT 61 E -> K (IN REF. 2).
SQ SEQUENCE 639 AA; 70933 MW; D3172DF94FF56AF5 CRC64;
Query Match 86.7%; Score 39; DB 1; Length 639;
Best Local Similarity 87.5%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNATEYFK 8
DB 293 NNHTFYFK 300
RESULT 3
TERT_OXTR STANDARD; PRT; 1132 AA.
ID TERT_OXTR STANDARD; PRT; 1132 AA.
AC 076332;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (telomerase catalytic
DE subunit) (telomerase subunit P133).
GN TERT.
OS Oxytricha trifallax.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Oxytricha.
OX NCBI_TaxID=5946;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337940; PubMed=9671703;
RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
RT "Telomerase reverse transcriptase genes identified in Tetrahymena
RT thermophila and Oxytricha trifallax".
RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).
CC -1- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR
CC THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT
CC ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS
CC SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE
CC SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY.
CC TELOMERASE SUBFAMILY.
CC
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 CC -----

DR EMBL: AF060230; AAC39163.1; -;
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PRO1365; TELOMERASE_RT.
 KW Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
 KW DNA-binding.
 SQ SEQUENCE 1132 AA; 134124 MW; 81E145F5F24392DC CRC64;

Query Match 80.0%; Score 35; DB 1; Length 1132;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 || :|||
 DB 1001 NNISFYFK 1008

RESULT 4
 CHLE_MOUSE
 ID CHLE_MOUSE STANDARD; PRT; 603 AA.

AC Q03311;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cholinesterase precursor (PC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudocholinesterase).
 GN BChE.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=90380429; PubMed=2400605;
 RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RA Bartels C.F., Noqueira C.P., la Du B.N., Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 RT butyrylcholinesterase from several vertebrates.";
 RL J. Biol. Chem. 266:6966-6974(1991).
 RN [2]

RP SEQUENCE OF 97-237 FROM N.A.

TISSUE=Liver;
 RX MEDLINE=91201348; PubMed=2016308;
 RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
 RA Bartels C.F., Noqueira C.P., la Du B.N., Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 RT butyrylcholinesterase from several vertebrates.";
 RL J. Biol. Chem. 266:6966-6974(1991).

CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.

CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
 CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.

CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS (EXCEPT ERYTHROCYTES).

CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.

CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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EMBL; M99492; AAA37328.1; -;
 DR PIR; A39768; A39768.
 DR HSSP; P21836; INAH.
 DR MGD; MGI:894278; Bche.
 DR InterPro; IPR002018; CarboxylesteraseB.

DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_estr_site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 603 CHOLINESTRASE.
 FT ACT_SITE 227 227 BY SIMILARITY.
 FT ACT_SITE 354 354 BY SIMILARITY.
 FT ACT_SITE 467 467 BY SIMILARITY.
 FT DISULFID 94 121 BY SIMILARITY.
 FT DISULFID 281 292 BY SIMILARITY.
 FT DISULFID 429 548 BY SIMILARITY.
 FT DISULFID 600 600 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 510 510 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 129 129 R -> P (IN REF. 2).
 SQ SEQUENCE 603 AA; 68521 MW; 719B1B220D1E5367 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 603;
 Best Local Similarity 85.7%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 7
 ||| |||
 DB 443 NNATFYFK 449

RESULT 5
 INVG_SALTY
 ID INVG_SALTY STANDARD; PRT; 562 AA.
 AC P35672;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE INVG protein precursor.
 GN INVG OR STM2898.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TMJ;
 RX MEDLINE=95172719; PubMed=7868245;
 RA Lodge J., Douce G.R., Amin I.I., Bolton A.J., Martin G.D.,
 RA Chaffield S., Dougan G., Brown N.L., Stephen J.;
 RT "Biological and genetic characterization of TphoA mutants of
 RT Salmonella typhimurium TML in the context of gastroenteritis.";
 RL Infect. Immun. 63:762-769(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SR-11;
 RX MEDLINE=95089692; PubMed=7997169;
 RA Kaniga K., Bossio J.C., Galan J.E.;
 RT "The Salmonella typhimurium invasion genes invF and invG encode
 RT homologues of the AraC and Ptd family of proteins.";
 RL Mol. Microbiol. 13:555-568(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Bante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
CC -!- FUNCTION: INVOLVED IN THE INVASION OF THE CELLS OF THE INTESTINAL
CC EPITHELIUM. COULD BE NECESSARY FOR THE EXPORT OF INVASION RELATED
CC DETERMINANTS.
CC -!- SUBCELLULAR LOCATION: Outer membrane (Potential).
CC -!- SIMILARITY: BELONGS TO THE PULD/OUTD/EXED/XPSD FAMILY.
CC -----
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CC -----
DR EMBL: X75302; CA53049.1; -;
DR EMBL: U08280; AA474040.1; -;
DR EMBL: AF008832; AAL21778.1; -;
DR PIR: S38422; S38422.
DR StyGene: SG10188; invG.
DR InterPro: IPR004846; GSPIL/IIIprotein.
DR InterPro: IPR004845; GSPILproteinC.
DR Pfam: PF00263; GSPIL_III; 1.
DR PROSITE: PS00875; T2SP_D; 1.
KW Virulence; Transport; Protein transport; Signal; Outer membrane;
KW Complete proteome.
FT SIGNAL 1 14 POTENTIAL.
FT CHAIN 15 562 INV G PROTEIN.
FT CONFLICT 12 12 A -> R (IN REF. 2).
FT CONFLICT 121 121 E -> Q (IN REF. 2).
FT CONFLICT 197 205 LRDKMWIP -> CAIRKWLFR (IN REF. 2).
FT CONFLICT 232 240 AMPAFSANG -> RCQRFORM (IN REF. 2).
FT CONFLICT 243 243 G -> S (IN REF. 2).
FT CONFLICT 262 264 AAA -> KPAEQ (IN REF. 2).
FT CONFLICT 328 328 S -> T (IN REF. 1 AND 2).
FT CONFLICT 329 329 I -> V (IN REF. 2).
FT CONFLICT 370 380 RPYLLTQENVP -> APGITSSGKGS (IN REF. 2).
SQ SEQUENCE 562 AA; 61765 MW; 8022905BE256058D CRC64;

Query Match 71.1%; Score 32; DB 1; Length 562;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|| ||| |
DB 385 NNRTFYTK 392

RESULT 6
NU5M_PIG STANDARD; PRT; 606 AA.
AC Q9TDR1.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
GN MTND5 OR ND5 OR NADH5.
OS Sus scrofa (Pig).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Landrace; TISSUE=Heart;
RX MEDLINE=99365306; PubMed=10433971;
RA Lin C.S., Sun Y.L., Liu C.Y., Yang P.C., Chang L.C., Cheng I.C.,
RA Mao S.J.T., Huang M.C.;
RT "Complete nucleotide sequence of pig (Sus scrofa) mitochondrial genome
and dating evolutionary divergence of pig within artiodactyla.";

RL Gene 236:107-114(1999).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----
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CC -----
DR EMBL: AF034253; AAD34195.1; -;
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR001516; Oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1; 1.
DR Pfam: PF00662; oxidored_q1_N; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 606 AA; 68649 MW; F5D6C256A41D284 CRC64;

Query Match 71.1%; Score 32; DB 1; Length 606;
Best Local Similarity 62.5%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
|| ||| |
DB 505 NNRTFYTK 512

RESULT 7
GCN2_YEAST STANDARD; PRT; 1590 AA.
AC P15442;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Protein kinase GCN2 (EC 2.7.1.-).
GN GCN2 OR ANS1 OR YDR283C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89282814; PubMed=2660141;
RA Wek R.C., Jackson B.M., Hinnebusch A.G.;
RT "Juxtaposition of domains homologous to protein kinases and histidyl-
RT tRNA synthetases in GCN2 protein suggests a mechanism for coupling
RT GCN4 expression to amino acid availability.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4579-4583(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=88261291; PubMed=3290651;
RA Rousou I., Thireos G., Hauge B.M.;
RT "Transcriptional-translational regulatory circuit in Saccharomyces
RT cerevisiae which involves the GCN4 transcriptional activator and the
RT GCN2 protein kinase.";
RL Mol. Cell. Biol. 8:2132-2139(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX Le T.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP ASSOCIATION WITH RIBOSOMES.
RX MEDLINE=91246169; PubMed=2038314;
RA Ramirez M., Wek R.C., Hinnebusch A.G.;
RT "Ribosome association of GCN2 protein kinase, a translational
RT activator of the GCN4 gene of Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 11:3027-3036(1991).
RN [5]
RP ACTIVITY ON SU12.
RX MEDLINE=92154672; PubMed=1739968;

RC STRAIN-Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: IGPS catalyzes the conversion of PPRF and glutamine to
 CC IGP, AICAR and glutamate. The hish subunit provides the glutamine
 CC amidotransferase activity that produces the ammonia necessary to
 CC hisf for the synthesis of IGP and AICAR (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-
 CC ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-
 CC carboxamide + L-glutamine -> imidazole-glycyl phosphate + 5-
 CC aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 CC -1- PATHWAY: Histidine biosynthesis; fifth step.
 CC -1- SUBUNIT: Heterodimer of hish and hisf (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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 CC
 CC EMBL; AP001118; BAB12822.1; .
 CC InterPro; IPR000991; GATase_1.
 CC Pfam; PF00117; GATase; 1.
 CC PROSITE; PS00442; GATASE_TYPE_I; FALSE_NEG.
 CC Histidine biosynthesis; Transferase; Glutamine amidotransferase;
 CC Complete proteome.
 CC ACT_SITE 77 BY SIMILARITY.
 CC ACT_SITE 178 BY SIMILARITY.
 CC ACT_SITE 180 BY SIMILARITY.
 CC SEQUENCE 196 AA; 21679 MW; 904624B74DBEBE5D CRC64;
 Query Match 68.9%; Score 31; DB 1; Length 196;
 Best Local Similarity 71.4%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NNATFYF 7
 Db 135 NNSRFYF 141
 RESULT 10
 U2AG_MOUSE STANDARD; PRT; 239 AA.
 ID Q9D883; Q9C998; Q99LX2;
 AC Q9D883; Q9C998; Q99LX2;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa
 DE subunit) (U2 snRNP auxiliary factor small subunit).
 GN U2AF1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Small intestine;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Akazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hilli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Wyshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE OF 2-239 FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-
 CC INTERACTIONS AND PROTEIN-RNA INTERACTIONS REQUIRED FOR ACCURATE 3/
 CC SPLICE SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN
 CC U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHANCERS AND
 CC THUS MAY FUNCTION AS A BRIDGE BETWEEN U2AF65 AND THE ENHANCER
 CC COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON (By similarity).
 CC -1- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN (By similarity).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (By similarity).
 CC -1- DOMAIN: The C-terminal SR-rich domain is required for
 CC interactions with SR proteins and the splicing regulators TRA and
 CC TRA2, and the N-terminal domain is required for formation of
 CC the U2AF35/U2AF65 heterodimer (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 CC -1- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
 CC -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AK008332; BAB25609.1; .
 CC EMBL; AK012849; BAB28511.1; .
 CC EMBL; BC002184; AAH02184.1; .
 CC MGD; MGI:98884; U2af1.
 CC InterPro; IPR000504; RNA_rec_mot.
 CC InterPro; IPR003954; RRM_1.
 CC InterPro; IPR000571; Znf_CCCH.
 CC Pfam; PF00076; rrm; 2.
 CC Pfam; PF00642; zf-CCCH; 4.
 CC SMART; SM00360; RRM; 1.
 CC SMART; SM00361; RRM; 1.
 CC SMART; SM00356; Znf_C3H1; 2.
 CC PROSITE; PS00102; RRM; 1.
 CC PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
 CC Nuclear protein; RNA-binding; mRNA splicing; Zinc-finger; Repeat.
 CC ZN_FING 13 41 C3H1-TYPE 1.
 CC ZN_FING 65 147 RNA-BINDING (RRM).
 CC ZN_FING 149 173 C3H1-TYPE 2.
 CC DOMAIN 179 238 ARG/GLY/SER-RICH (RS DOMAIN).
 CC CONFLICT 187 187 G -> R (IN REF. 1; BAB25609).
 CC SEQUENCE 239 AA; 27815 MW; DPF944210581244D CRC64;
 Query Match 68.9%; Score 31; DB 1; Length 239;
 Best Local Similarity 71.4%; Pred. No. 46;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 NATFYF 8
 Db 17 NCSFYF 23

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. BINDS TO THE
 CC POLYPYRIMIDINE TRACT OF INTRONS EARLY DURING SPLICOSOME ASSEMBLY
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 CC -1- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
 CC -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U67066; AAB17271.1; -;
 DR EMBL; AE003590; AAF51512.1; -;
 DR FlyBase; FBgn0017457; U2af38.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR InterPro; IPR003954; RRM_1.
 DR InterPro; IPR000571; Znf_CCHC.
 DR Pfam; PF00076; rrm; 1.
 DR Pfam; PF00642; zf-CCCH; 2.
 DR SMART; SM00356; Znf_C3H1; 1.
 DR SMART; SM00356; Znf_C3H1; 2.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
 KW Nuclear protein; RNA-binding; mRNA splicing; zinc-finger; Repeat.
 FT DOMAIN 44 149 RNA-BINDING (RRM).
 FT DOMAIN 180 213 ARG/SER-RICH (RS DOMAIN).
 FT DOMAIN 190 197 POLY-ARG.
 FT DOMAIN 252 262 POLY-GLY.
 FT CONFLICT 66 66 H -> D (IN REF. 1).
 SQ SEQUENCE 264 AA; 23877 MW; 577285FB6FDB2F5 CRC64;
 Query Match 68.9%; Score 31; DB 1; Length 264;
 Best Local Similarity 71.4%; Pred. No. 50;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 NATFYFK 8
 DB 17 NCSFYFK 23
 RESULT 13
 ID ARG_C_ECOLI STANDARD; PRT; 334 AA.
 AC P11446;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
 DE acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
 GN ARG_C OR B3958.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=891121510; PubMed=2851495;
 RA Parsot C., Boyen A., Cohen G.N., Glansdorff N.;
 RT "Nucleotide sequence of *Escherichia coli* argB and argC genes:
 RT comparison of N-acetylglutamate kinase and
 RT N-acetylglutamate-gamma-semialdehyde dehydrogenase with homologous
 RL and analogous enzymes.";
 RL Gene 68:275-283(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MGI655;
 RX MEDLINE=94089392; PubMed=8265357;
 RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the *Escherichia coli* genome. IV. DNA sequence of the
 RT region from 89.2 to 92.8 minutes.";
 RL Nucleic Acids Res. 21:5408-5417(1993).
 RN [3]
 RP SEQUENCE OF 1-48 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=83143275; PubMed=6761650;
 RA Plette J., Cunin R., Boyen A., Charlier D.R.M., Crabeel M.,
 RA van Vliet F., Glansdorff N., Squires C., Squires C.L.;
 RT "The regulatory region of the divergent *argECBH* operon in *Escherichia*
 RT *coli* K-12.";
 RL Nucleic Acids Res. 10:8031-8048(1982).
 RN [4]
 RP SEQUENCE OF 1-19 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92202162; PubMed=1551850;
 RA Meinel T., Schmitt E., Mechulam Y., Blanguet S.;
 RT "Structural and biochemical characterization of the *Escherichia coli*
 RT *argE* gene product.";
 RL J. Bacteriol. 174:2323-2331(1992).
 CC -1- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+) + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
 CC -1- PATHWAY: Arginine biosynthesis; third step.
 CC -1- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M21446; AAA23477.1; -;
 DR EMBL; J01587; AAB59146.1; -;
 DR EMBL; X55417; -; NOT_ANNOTATED_CDS.
 DR EMBL; U00006; AAC43064.1; -;
 DR EMBL; AE000470; AAC76940.1; -;
 DR PIR; J01332; RDECEP.
 DR EcoGene; EG10065; argC.
 DR InterPro; IPR000706; AGPR_act_site.
 DR InterPro; IPR000534; Semialdh_dh.
 DR Pfam; PF01118; Semialdh_dh; 1.
 DR Pfam; PF02774; Semialdh_dh; 1.
 DR ProDom; PD003765; AGPR_act_site; 1.
 DR PROSITE; PS01224; ARG_C; 1.
 DR Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT ACT_SITE 154 154 BY SIMILARITY.
 SQ SEQUENCE 334 AA; 35952 MW; 67AC195ECE1C4789 CRC64;

Query Match 68.9%; Score 31; DB 1; Length 334;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 NNATYFK 8
DB 109 NDATYFK 116

RESULT 14
ID OMPU_VIBCH STANDARD; PRT; 341 AA.
AC P97085; Q9L5A3; Q9KU90;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Outer membrane protein U precursor (Porin ompU).
GN OMPU OR VC0633.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Classical Ogawa 395 / ATCC 39541 / Serotype O1;
RX MEDLINE-97101069; PubMed-8945596;
RA Sperandio V., Bailey C.C., Giron J.A., Dirita V.J., Silveira W.D.,
RA Vettore A.L., Kaper J.B.;
RT "Cloning and characterization of the gene encoding the ompU outer
membrane protein of Vibrio cholerae.";
RL Infect. Immun. 64:5406-5409(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor;
RA Yin Y., Zhang J.Z.;
RT "Cloning and expression of ompU of Vibrio cholerae and its
antigenicity analysis.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE-20406833; PubMed-10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.B., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RL Nature 406:477-483(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
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CC EMBL; U73751; ABA48973.1; ..
DR EMBL; AF253529; AAF64526.1; ..
DR EMBL; AE004149; AAF93799.1; ALT_INIT.
DR TIGR; VC0633; ..
DR InterPro; IPR003229; OMP_2.
DR InterPro; IPR001702; Porin_gram-ve.
DR Pfam; PF00267; Gram-ve_porins; 1.
KW Transmembrane; Porin; Signal; Outer membrane; Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 341 OUTER MEMBRANE PROTEIN U.
FT CONFLICT 278 278 F -> I (IN REF. 2).
FT CONFLICT 290 290 E -> K (IN REF. 1).

FT CONFLICT 324 325 VG -> AS (IN REF. 1).
SQ SEQUENCE 341 AA; 36645 MW; CECB39070E441732 CRC64;

Query Match 68.9%; Score 31; DB 1; Length 341;
Best Local Similarity 71.4%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATYFK 8
DB 299 DATYFK 305

RESULT 15
ID KNL2_BOVIN STANDARD; PRT; 434 AA.
AC P01047;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kininogen, LMW II precursor (Thiol proteinase inhibitor) [Contains:
DE Bradykinin].
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-83117859; PubMed-6572010;
RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
RT "Primary structures of bovine liver low molecular weight kininogen
precursors and their two mRNAs.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
RN [2]
RP SEQUENCE OF 19-376.
RX MEDLINE-87137530; PubMed-3546295;
RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA Miyata T., Iwanaga S.;
RT "Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
chain portion.";
RL J. Biol. Chem. 262:2768-2779(1987).
CC -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOLESTERASES; (2)
LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LMW-KININOGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (3B) INDUCTION OF HYPOTENSION, (3C)
NATRIURESIS AND DIURESIS (KIDNEY).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; LMW II (shown here) and HMW II
(AC P01045); are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
CC -1- MISCELLANEOUS: LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
INVOLVED IN BLOOD CLOTTING.
CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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CC EMBL; V00427; CAA23710.1; ..
DR PIR; A01284; KGBOL2.
DR HSSP; P01038; 1A90.
DR InterPro; IPR000010; Cystatin.
DR Pfam; PF000031; cystatin; 3.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

KW Thiol protease inhibitor; Bradykinin; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 434 KININOGEN, LMW II.
 FT CHAIN 19 376 HEAVY CHAIN.
 FT PEPTIDE 378 386 BRADYKININ.
 FT CHAIN 387 434 LIGHT CHAIN.
 FT DOMAIN 19 135 CYSTATIN-LIKE 1.
 FT DOMAIN 136 256 CYSTATIN-LIKE 2.
 FT DOMAIN 257 376 CYSTATIN-LIKE 3.
 FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 136 136 O-LINKED (PARTIAL).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .); OR 169.
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (PARTIAL).
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).
 FT DISULFID 27 404 INTERCHAIN.
 FT DISULFID 82 93
 FT DISULFID 106 125
 FT DISULFID 141 144
 FT DISULFID 205 217
 FT DISULFID 228 247
 FT DISULFID 261 264
 FT DISULFID 325 337
 FT DISULFID 348 367
 SQ SEQUENCE 434 AA; 48148 MW; 73A7079DE3E03430 CRC64;

Query Match 68.9%; Score 31; DB 1; Length 434;
 Best Local Similarity 62.5%; Pred. No. 83;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 :: |||||
 Db 290 HDGTFYFK 297

Search completed: March 13, 2003, 19:13:24
 Job time : 6 secs

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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:27 ; Search time 16.6667 Seconds
(without alignments)
98.903 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATFFYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTEMBL-21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp Vertebrate.*
- 15: sp Unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 18: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	80.0	858	5 Q21853	Q21853 caenorhabdi
2	35	77.8	182	5 Q21968	Q21968 caenorhabdi
3	35	77.8	628	16 Q8RI47	Q8RI47 fusobacteri
4	34	75.6	71	16 Q9KDI7	Q9KDI7 bacillus ha
5	34	75.6	115	15 Q9YXT3	Q9YXT3 human immun
6	34	75.6	173	10 Q9ZRF8	Q9ZRF8 oryza sativ
7	34	75.6	181	10 Q9M625	Q9M625 hordeum vul
8	34	75.6	182	10 Q93615	Q93615 triticum ae
9	34	75.6	273	16 Q9CD90	Q9CD90 mycobacteri
10	34	75.6	319	16 Q9CJ05	Q9CJ05 lactococcus
11	34	75.6	326	12 Q66771	Q66771 equine rota
12	34	75.6	326	12 Q66772	Q66772 equine rota
13	34	75.6	326	12 Q91E87	Q91E87 human rotav
14	34	75.6	357	13 Q91655	Q91655 xenopus lae
15	34	75.6	440	8 Q9ZY23	Q9ZY23 pedinomonas
16	34	75.6	497	10 Q9FVS9	Q9FVS9 arabidopsis

17	34	75.6	590	17 Q8U306	Q8U306 pyrococcus
18	34	75.6	599	16 Q8XP19	Q8XP19 clostridium
19	34	75.6	602	2 Q9AFA2	Q9AFA2 staphylococ
20	34	75.6	630	5 P91391	P91391 caenorhabdi
21	34	75.6	758	5 O16610	O16610 caenorhabdi
22	34	75.6	949	16 Q97DN1	Q97DN1 clostridium
23	33	73.3	251	10 Q9LDL9	Q9LDL9 arabidopsis
24	33	73.3	303	5 O44623	O44623 caenorhabdi
25	33	73.3	332	10 O64597	O64597 arabidopsis
26	33	73.3	469	17 O29037	O29037 archaeoglob
27	33	73.3	599	2 Q8VNV4	Q8VNV4 clostridium
28	33	73.3	613	12 Q8QNM5	Q8QNM5 ectocarpus
29	33	73.3	706	10 Q9S7L6	Q9S7L6 arabidopsis
30	33	73.3	1346	5 O45699	O45699 caenorhabdi
31	32	71.1	155	8 O79080	O79080 lipolexis g
32	32	71.1	331	12 Q91AP3	Q91AP3 human rotav
33	32	71.1	512	8 Q8WHL8	Q8WHL8 lemma japon
34	32	71.1	537	10 Q9LH23	Q9LH23 oryza sativ
35	32	71.1	562	16 Q8Z489	Q8Z489 salmonella
36	32	71.1	567	16 Q8X6D6	Q8X6D6 escherichia
37	32	71.1	606	8 Q9GIW4	Q9GIW4 sus scrofa
38	32	71.1	606	8 Q99997	Q99997 sus scrofa
39	32	71.1	606	8 Q9G7T6	Q9G7T6 sus scrofa
40	32	71.1	606	8 Q9G7R8	Q9G7R8 sus scrofa
41	32	71.1	630	12 Q9EML1	Q9EML1 amsacta moo
42	32	71.1	744	12 Q8V7G0	Q8V7G0 tt virus. o
43	32	71.1	1096	4 O94836	O94836 homo sapien
44	32	71.1	1191	5 Q9VJN7	Q9VJN7 drosophila
45	32	71.1	1215	5 Q22649	Q22649 caenorhabdi

ALIGNMENTS

RESULT 1

Q21853	ID	Q21853	PRELIMINARY;	PRT;	858 AA.
AC	Q21853;				
DT	01-NOV-1996	(TEMBLrel. 01, Created)			
DT	01-NOV-1996	(TEMBLrel. 01, Last sequence update)			
DT	01-DEC-2001	(TEMBLrel. 19, Last annotation update)			
DE	R09A8.2	protein.			
GN	R09A8.2.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxID=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Wilkinson J.;				
RL	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99069613; PubMed=9851916;				
RA	none;				
RT	"Genome sequence of the nematode C.elegans: A platform for				
RT	investigating biology."				
RL	Science 282:2012-2018(1998).				
DR	EMBL; Z68009; CAA92004.1; ..				
SQ	SEQUENCE 858 AA; 96262 MW; 60E1070CA8F4D4C8 CRC64;				

Query Match 80.0%; Score 36; DB 5; Length 858;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYFK 8
| :|||||
Db 49 NESTFFYFK 56

RESULT 2

Q21968	ID	Q21968	PRELIMINARY;	PRT;	182 AA.
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Q21968;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE R12H7.3 protein.
 GN R12H7.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Colles L.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z50755; CAA90635.1; -.
 DR InterPro: IPR001232; Skp1.
 DR Pfam: PF01466; Skp1; 1.
 DR SMART; SM00512; Skp1; 1.
 SQ SEQUENCE 182 AA; 21178 MW; 4BE38A19C4FA8124 CRC64;

Query Match 77.8%; Score 35; DB 5; Length 182;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 ||||:|
 Db 161 NNATLFFK 168

RESULT 3
 Q8RI47
 ID Q8RI47 PRELIMINARY; PRT; 628 AA.
 AC Q8RI47;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Tetrairicopeptide repeat family protein.
 GN FN1787.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21186394; PubMed=11889109;
 RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Feinstein M., Kyripides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AE010481; AAL93886.1; -.
 KW Complete proteome.
 SQ SEQUENCE 628 AA; 73857 MW; 013321316E4829B4 CRC64;

Query Match 77.8%; Score 35; DB 16; Length 628;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 ||||:|
 Db 127 NNASYFK 134

RESULT 4
 Q9KDI7
 ID Q9KDI7 PRELIMINARY; PRT; 71 AA.
 AC Q9KDI7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein BH1226.
 GN BH1226.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001511; BAB04945.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 71 AA; 8026 MW; 311AC9AEB3C539D3 CRC64;

Query Match 75.6%; Score 34; DB 16; Length 71;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFYF 7
 |||||
 Db 43 NATFYF 48

RESULT 5
 Q9YXT3
 ID Q9YXT3 PRELIMINARY; PRT; 115 AA.
 AC Q9YXT3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Envelope glycoprotein C2V3 region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RJ96BRP071;
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
 RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
 RA Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."
 RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF034019; AAC79271.1; -.
 DR InterPro: IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein.
 KW NON_TER 1
 FT NON_TER 115
 SQ SEQUENCE 115 AA; 12755 MW; 6551E67B32DCF56C CRC64;

Query Match 75.6%; Score 34; DB 15; Length 115;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 ||||:|
 Db 78 NNATFFFR 85

```

RESULT 6
ID Q9ZRF8 PRELIMINARY; PRT; 173 AA.
AC Q9ZRF8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hydrophobic LEA-like protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LONELLO;
RA Chen L.J., Chai Y.J., Chen P.W.;
RT "A rice embryo-specific gene with high homology to soybean GmPM3 gene,
RL a hydrophobic LEA protein gene.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57639; AAD10377.1;
SQ SEQUENCE 173 AA; 18287 MW; 63FA2F778BB7259D CRC64;

Query Match 75.6%; Score 34; DB 10; Length 173;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
Db 47 NGATFFYF 53

RESULT 7
ID Q9M625 PRELIMINARY; PRT; 181 AA.
AC Q9M625;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Plasma membrane associated protein.
GN PM19.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Morris P.C., Ranford J.C.;
RT "Hordeum vulgare hydrophobic embryo-associated protein PM19 mRNA.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218627; AAP29532.1;
SQ SEQUENCE 181 AA; 19036 MW; 849727F1123A4030 CRC64;

Query Match 75.6%; Score 34; DB 10; Length 181;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
Db 47 NGATFFYF 53

RESULT 8
ID P93615 PRELIMINARY; PRT; 182 AA.
AC P93615;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ABA induced plasma membrane protein PM 19.
GN WTABAPM.
OS Triticum aestivum (Wheat).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CHIHOKU;
RX MEDLINE=97393494; PubMed=9249988;
RA Koike M., Takezawa D., Arakawa K., Yoshida S.;
RT "Accumulation of 19-kDa plasma membrane polypeptide during induction
RT of freezing tolerance in wheat suspension-cultured cells by abscisic
RT acid.";
RL Plant Cell Physiol. 38:707-716(1997).
DR EMBL; U80037; AAB38504.1;
SQ SEQUENCE 182 AA; 19009 MW; 799B9994AEA87DCB CRC64;

Query Match 75.6%; Score 34; DB 10; Length 182;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
Db 47 NGATFFYF 53

RESULT 9
ID Q9CD90 PRELIMINARY; PRT; 273 AA.
AC Q9CD90;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein ML0126.
GN ML0126.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AJ583917; CAC29634.1;
DR Leproma; ML0126;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 273 AA; 30831 MW; D5B765A65EF39549 CRC64;

Query Match 75.6%; Score 34; DB 16; Length 273;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFFYF 7
Db 20 NNAQFFYF 26

RESULT 10
ID Q9CJ05 PRELIMINARY; PRT; 319 AA.
AC Q9CJ05;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Rhamnosyitransferrase.
GN RGPB OR LL0201.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacilliales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR4;
RX MEDLINE=95113986; PubMed=11337471;
RA Bolotin A., Wincker P., Mauer S., Jaillon O., Malarne K.,
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis I1403."
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006258; AAK04299.1; -.
DR HSSP; P39621; LOGO.
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Transferrase; Complete proteome.
SQ SEQUENCE 319 AA; 37340 MW; D1DAC78AB0A950CA CRC64;

Query Match 75.6%; Score 34; DB 16; Length 319;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYF 7
DB 80 NNADYF 86

RESULT 11
Q66771 Q66771 PRELIMINARY; PRT; 326 AA.
ID AC Q66771;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Glycoprotein VP7.
OS Equine rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR4;
RX MEDLINE=95113988; PubMed=7814511;
RA Claret M., Reggati F., Pina C.I., Liprandi F.;
RT "Equine rotaviruses with G14 serotype specificity circulate among
RT Venezuelan horses."
RL J. Clin. Microbiol. 32:2609-2612(1994).
DR EMBL; U05348; AAA81914.1; -.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
SQ SEQUENCE 326 AA; 37296 MW; 9FC1BD4F4CC76529 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYF 8
DB 318 NSATFYR 325

RESULT 12
Q66772 Q66772 PRELIMINARY; PRT; 326 AA.
ID AC Q66772;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Gene 17 protein.

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DE Glycoprotein VP7.
OS Equine rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR8;
RX MEDLINE=95113988; PubMed=7814511;
RA Claret M., Reggati F., Pina C.I., Liprandi F.;
RT "Equine rotaviruses with G14 serotype specificity circulate among
RT Venezuelan horses."
RL J. Clin. Microbiol. 32:2609-2612(1994).
DR EMBL; U05349; AAA67342.1; -.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
SQ SEQUENCE 326 AA; 37352 MW; 9095E64B13933E29 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYF 8
DB 318 NSATFYR 325

RESULT 13
Q91E87 Q91E87 PRELIMINARY; PRT; 326 AA.
ID AC Q91E87;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Capsid protein.
GN VP7.
OS Human rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CC425;
RA Griffin D.D., Nakagomi T., Hoshino Y., Nakagomi O., Kirkwood C.D.,
RA Parashar U.D., Glass R.I., Gentsch J.R.;
RT "Characterization of nontypeable rotavirus strains from the United
RT States: Identification of a new rotavirus reassortant (P2a[6],G12) and
RT rare P3[9] strains related to bovine rotaviruses."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311738; CAC43312.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SQ SEQUENCE 326 AA; 37119 MW; 8B97ED1DBBDC981 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYF 8
DB 318 NSATFYR 325

RESULT 14
Q91655 Q91655 PRELIMINARY; PRT; 357 AA.
ID AC Q91655;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Gene 17 protein.

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GN GENE 17.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312514; PubMed=8700860;
RA Brown D.D., Wang Z., Furlow J.D., Kanamori A., Schwartzman R.A.,
RA Remo B.F., Pinder A.;
RT "The thyroid hormone-induced tail resorption program during Xenopus
RT laevis metamorphosis";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929(1996).
DR EMBL; U41860; AAC59876.1; -;
DR InterPro; IPR001507; Endoglin/CD105.
DR Pfam; PF00100; zona_pellucida; 1.
DR SMART; SM00241; ZP; 1.
SQ SEQUENCE 357 AA; 39090 MW; 5493352C8EEA21E6 CRC64;

Query Match 75.6%; Score 34; DB 13; Length 357;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYF 7
DB 141 NNATLYF 147

RESULT 15
Q9ZY23 PRELIMINARY; PRT; 440 AA.
AC Q9ZY23;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 2 (EC 1.6.5.3).
GN NAD2.
OS Pedinomonas minor.
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Chlorophyta; Pedinophyceae; Pedinomonadales;
OC Pedinomonadaceae; Pedinomonas.
OX NCBI_TaxID=3159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX LB 1350;
RX MEDLINE=99418884; PubMed=10488238;
RA Turnel M., Lemieux C., Burger G., Lang B.F., Otis C., Plante I.,
RA Gray M.W.;
RT "The complete mitochondrial DNA sequences of Nephroselmis olivacea and
RT Pedinomonas minor: two radically different evolutionary patterns
RT within green algae";
RL Plant Cell 11:1717-1729(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UTEX LB 1350;
RA Burger G.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF116775; AAD19671.1; -;
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; Oxidored_q1; 1.
DR Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 440 AA; 51380 MW; C6D6CBAD72549B4C CRC64;

Query Match 75.6%; Score 34; DB 8; Length 440;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYF 7
DB 238 NNATLYF 244

Search completed: March 13, 2003, 19:13:02
Job time : 18.6667 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:07 ; Search time 42 Seconds
(without alignments)
50.762 Million cell updates/sec

Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNATFFYFKIDNVKKAR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	100.0	16	21	AAV95410
2	84	100.0	32	21	AAV95408
3	84	100.0	117	14	AAK33350
4	84	100.0	122	21	AAK37447
5	84	100.0	123	21	AAV95426
6	84	100.0	248	22	ABG21102
7	84	100.0	369	22	ABG21099
8	84	100.0	626	23	ABK78707
9	84	100.0	644	22	ABG21101
10	84	100.0	644	23	ABK78710

11	78	92.9	26	18	AAW54336	Bradykinin analogo
12	70	83.3	435	22	ABG21105	Novel human diago
13	59	70.2	434	5	AAK40633	Bradykinin protein
14	57	67.9	16	21	AAK08553	Peptide identified
15	56	66.7	235	23	ABG60077	Human DTHP polype
16	54	64.3	436	5	AAK40257	Human DTHP polype
17	49	58.3	9	21	AAK37455	Bradykinin protein
18	45	53.6	10	21	AAV95405	Human kininogen D3
19	45	53.6	16	21	AAV95409	Anti-angiogenic D3
20	45	53.6	554	23	ABP27632	Streptococcus poly
21	44	52.4	867	20	AAV34508	Streptococcus poly
22	44	52.4	875	20	AAV34381	Streptococcus poly
23	44	51.2	466	23	ABK48663	Porphyromonas ging
24	41	48.8	872	23	ABK77619	Listeria monocytog
25	41	48.8	996	23	ABK91160	AMEPV mRNA capping
26	40	47.6	74	22	AAO60226	Herbicidally activ
27	40	47.6	152	21	AAO32794	Human polypeptide
28	40	47.6	133	21	AAO32793	Zea mays protein f
29	40	47.6	186	21	AAO32792	Zea mays protein f
30	40	47.6	179	21	AAV32469	DNA encoding fellin
31	40	47.6	1191	22	ABK60775	Drosophila melanog
32	39	46.4	12	21	AAV95407	Anti-angiogenic pe
33	39	46.4	701	21	AAV51007	C. vicina LSP-2 pr
34	38	45.2	40	23	AAU89265	Insulin/insulin-li
35	38	45.2	42	22	AAK74378	Human colon cancer
36	38	45.2	44	23	AAU90767	Insulin/insulin-li
37	38	45.2	121	21	AAV81200	Human mutant cysta
38	38	45.2	128	21	AAV81189	Human mutant cysta
39	38	45.2	156	18	AAK20537	H. pylori cytoplas
40	38	45.2	222	21	AAK52576	Helicobacter pylor
41	38	45.2	277	23	ABK51474	Human MDDT SEQ ID
42	38	45.2	282	22	AAK92301	C glutamicum prote
43	38	45.2	316	22	AAK62195	Drosophila melanog
44	38	45.2	345	18	AAK20757	H. pylori cytoplas
45	38	45.2	360	23	ABK92315	Herbicidally activ

ALIGNMENTS

RESULT 1
AAV95410
ID AAV95410 standard; Peptide; 16 AA.

XX AAV95410;
XX
XX
XX 25-SEP-2000 (first entry)
XX
XX Anti-angiogenic D3 peptide.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
XX endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW rheumatoid arthritis; cytostatic; antirheumatic;
KW therapy; human; D3 peptide.

XX Homo sapiens.
XX
XX WO200035407-A2.
XX
XX 22-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US28465.
XX
XX 16-DEC-1998; 98US-0112427.
XX
XX (UTEM) UNIV TEMPLE.
XX (MCCR/) MCCRAE R K.
XX
XX McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell

PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 PT 3 analog

PS Claim 7; Page 26; 44pp; English.

XX The present sequence is that of a D3 peptide derived from human
 CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell
 CC proliferation.

XX Sequence 16 AA;

Query Match 100.0%; Score 84; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.4e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKAR 16

DB 1 NNATFFFKIDNVKKAR 16

RESULT 2

AAY95408
 ID AAY95408 standard; Peptide; 32 AA.

AC AAY95408;

DT 25-SEP-2000 (first entry)

DE Anti-angiogenic D3 peptide.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.

XX Homo sapiens.

OS WO200035407-A2.

PN 22-JUN-2000.

PD 02-DEC-1999; 99WO-US28465.

PF 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.

PA (MCCR/) MCCRAE R K.

XX McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell
 PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 PT 3 analog

PS Claim 4; Page 26; 44pp; English.

XX The present sequence is that of a D3 peptide derived from human

CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys282.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.

XX Sequence 32 AA;

Query Match 100.0%; Score 84; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 3e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKAR 16

DB 13 NNATFFFKIDNVKKAR 28

RESULT 3

AAR33350
 ID AAR33350 standard; protein; 117 AA.

AC AAR33350;

DT 01-JUL-1993 (first entry)

DE Domaine 3, bradykinin release activating peptide.

XX Domain 3; human; kininogen; heavy chain; low molecular weight; plasma;
 KW trypsin; platelet; activation; granule contents; hemostasis; thrombin;
 KW tissue plasminogen activator; thrombosis; inflammatory response;
 KW endothelial cell; von Willebrand factor;

XX Homo sapiens.

OS Key Location/Qualifiers

PH Peptide 1..18 /note= "Leader peptide"

FT Protein 19..117 /note= "Mature protein"

XX WO9303748-A.

XX 04-MAR-1993.

XX 13-AUG-1992; 92WO-US06809.

XX 13-AUG-1991; 91US-0744545.

XX (UTEM) UNIV TEMPLE.

XX Jiang Y, Schmaier AB;

XX WPI; 1993-093714/11.

XX Use of trypsin-cleavage fragment of human kininogen - for
 PT increasing vascular bradykinin release, for lowering blood
 PT pressure and treating hypertension

XX Disclosure; Fig 1; 46pp; English.

XX The sequence given represents domain 3, amino acids 246-362, of
 CC the human kininogen heavy chain. Domain 3 was isolated from low
 CC molecular weight kininogen, derived from human plasma, by cleavage
 CC with trypsin. Domain 3 peptide inhibits platelet activation causing
 CC a marked decrease in the platelets ability to aggregate and secrete
 CC their granule contents. The granule contents comprise proteins which
 CC participate in hemostasis, thrombosis and the inflammatory response.

CC Domain 3 also inhibits endothelial cell activation shown by a decrease
CC in secretion of endothelial cell contents such as tissue plasminogen
CC activator and von Willebrand factor. Domain 3 functions to inhibit
CC cell activation by blocking thrombin binding to its target cells, the
CC peptide is a selective inhibitor of thrombin-induced platelet
CC activation.
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 84; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKAR 16
| | | | | | | | | | | | | | | |
Db 30 NNATFFFKIDNVKKAR 45

RESULT 4
AAB37447
ID AAB37447 standard; protein; 122 AA.

AC AAB37447;

DT 21-FEB-2001 (first entry)

XX Human kininogen D3.

XX Enzyme; legumain; endopeptidase; cystatin; human; kininogen.

XX Homo sapiens.

OS WO200064945-A1.

PN 02-NOV-2000.

XX 20-APR-2000; 2000WO-GB01571.

XX 22-APR-1999; 99GB-0009133.

XX (BABR-) BABRAHAM INST.

XX Abrahamson M, Barrett AJ;

XX WPI; 2000-687316/67.

XX Inhibition of mammalian legumain or legumain-related endopeptidase by
PT cystatin involves interaction with second papain-non-reactive site of
PT cystatin -

XX Disclosure; Fig 4; 45pp; English.

XX The present invention relates to inhibition of the enzymatic activity of
CC legumain or a legumain-related endopeptidase by cystatin. The inhibition
CC involves an interaction between legumain and a papain-non-reactive site
CC of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
CC performs a protein-processing function. The present sequence is human
CC kininogen D3, which was used in the present invention. Kininogen is a
CC type 3 cystatin.

XX Sequence 122 AA;

Query Match 100.0%; Score 84; DB 21; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKAR 16
| | | | | | | | | | | | | | | |
Db 35 NNATFFFKIDNVKKAR 50

RESULT 5
AAY95426

ID AAY95426 standard; Peptide; 123 AA.

XX AAY95426;

XX 25-SEP-2000 (first entry)

XX Human high mol.wt. kininogen domain 3.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
KW rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic;
KW therapy; human; D3 peptide.

XX Homo sapiens.

XX WO200035407-A2.

XX 22-JUN-2000.

XX 02-DEC-1999; 99WO-US28465.

XX 16-DEC-1998; 98US-0112427.

XX (UTEM) UNIV TEMPLE.

PA (MCCR/) MCCRAE R K.

XX McCrae RK;

XX WPI; 2000-442247/38.

XX Composition for inhibiting angiogenesis and endothelial cell
PT proliferation, inducing endothelial cell apoptosis and treating cancer,
PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
PT 3 analog -

XX Disclosure; Page 4; 44pp; English.

XX The present sequence is that of domain 3 of human high mol.wt.
CC kininogen (HK). The invention provides peptides (see AAY95405-24)
CC that are analogues of certain sites in the HK domain 3.

CC specifically Asn275-Lys282, Cys246-Cys249, Leu331-Tyr338 and
CC Tyr299-Ser314. The peptides, in which native Cys residues may be
CC replaced by Ala residues, inhibit endothelial cell proliferation
CC and may also induce endothelial cell apoptosis. Compositions
CC including the peptides are used in claimed methods for inhibiting
CC angiogenesis, inhibiting endothelial cell proliferation, and
CC inducing endothelial cell apoptosis. Cancer, rheumatoid arthritis,
CC and ocular disorders characterized by undesired vascularization of
CC the retina are treated.

XX Sequence 123 AA;

Query Match 100.0%; Score 84; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFFKIDNVKKAR 16
| | | | | | | | | | | | | | | |
Db 41 NNATFFFKIDNVKKAR 56

RESULT 6
ABG21102
ID ABG21102 standard; Protein; 248 AA.

XX ABG21102;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #21093.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; NAs85289.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX PS Claim 20; SEQ ID NO 51461; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 248 AA;
 Query Match 100.0%; Score 84; DB 22; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNATFYFKIDNVKKAR 16
 |||||
 Db 90 NNATFYFKIDNVKKAR 105

RESULT 7
 ABG21099
 ID ABG21099 standard; Protein; 369 AA.
 XX AC ABG21099;
 XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #21090.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.

XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; NAs85286.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX PS Claim 20; SEQ ID NO 51458; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 369 AA;
 Query Match 100.0%; Score 84; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NNATFYFKIDNVKKAR 16
 |||||
 Db 333 NNATFYFKIDNVKKAR 348

RESULT 8
 ABB78707
 ID ABB78707 standard; Protein; 626 AA.
 XX AC ABB78707;
 XX DT 18-JUL-2002 (first entry)

XX DE Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1.
 XX KW Human; kininogen; high molecular weight kininogen; HK; D5 domain;
 XX KW D5 receptor; angiotensin; endothelial cell; cytostatic; antitumour;
 XX KW antithrombotic; vasotrophic; vulnerable; tranquilliser; thrombolytic;
 XX KW ophthalmological; gynaecological; antiulcer; antidiabetic; antiarthritic;
 XX KW antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.

OS Homo sapiens.
XX Key Location/Qualifiers
FH Domain 384..508
FT /label= D5_domain
XX
PN WO200214369-A2.
XX
PD 21-FEB-2002.
XX
XX 24-JUL-2001; 2001WO-US23185.
PF
XX 24-JUL-2000; 2000US-220194P.
PR
XX (ATTE-) ATTENUON LLC.
PA
XX Mazar AP, Juarez JC;
PI
XX WPI; 2002-393611/42.
DR
XX Novel human kininogen D5 domain polypeptides useful for treating
PT conditions associated with endothelial cell migration, proliferation,
PT invasion or angiogenesis, e.g. arthritis, macular degeneration, benign
PT hyperplasia
XX
PS Disclosure; Page 13; 84pp; English.
XX
CC The present invention describes an isolated polypeptide (I) that
CC corresponds to the D5 domain of human kininogen, or biologically active
CC peptide fragment, homologue or functional derivative, and which:
CC (a) inhibits angiogenesis; (b) binds to the D5 binding site on
CC endothelial cells (EC); (c) activates signalling pathways leading to the
CC introduction of apoptosis in EC; and/or (d) inhibits the signalling
CC pathway required for maintenance of EC viability. (I) has cytostatic,
CC antitumour, antiatherosclerotic, vasotropic, vulnary, tranquilliser,
CC thrombolytic, ophthalmological, gynaecological, antiulcer, antidiabetic,
CC antiarthritic, antiangiogenic, antiapoptotic and endocrine activities.
CC An antibody (IX) specific for an epitope of (I) is useful for inhibiting
CC tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide
CC (II) or a dimeric or trimeric fusion polypeptide (III) can be used for
CC inhibiting EC migration, proliferation, invasion, or angiogenesis, or
CC for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical
CC composition (X) comprising (I), (II), or (III), can be used for treating
CC a subject having a disease or condition associated with undesired EC
CC migration, proliferation, invasion or angiogenesis. (I), (II), or (III)
CC can be used for isolating a D5 domain binding molecule from a complex
CC mixture and for isolating or enriching cells expressing D5 domain binding
CC sites from a cell mixture. The present sequence represents the mature
CC human high molecular weight kininogen (HK) protein, which is given in
CC the exemplification of the present invention.
XX
SQ Sequence 626 AA;
Query Match 100.0%; Score 84; DB 23; Length 626;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNATFFFKIDNVKKAR 16
| | | | | | | | | | | | | | | | | |
Db 275 NNATFFFKIDNVKKAR 290
RESULT 9
ID ABG21101
XX ABG21101 standard; Protein; 644 AA.
XX
AC ABG21101;
XX
XX 18-FEB-2002 (first entry)
DT
XX Novel human diagnostic protein #21092.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW

KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX WO200175067-A2.
XX
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-MAR-2000; 2000US-0540217.
PR
XX 23-AUG-2000; 2000US-0649167.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
PI
XX N-PSDB; AAS85288.
DR
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
XX Claim 20; SEQ ID No 51460; 103pp; English.
PS
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 644 AA;
SQ
Query Match 100.0%; Score 84; DB 22; Length 644;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNATFFFKIDNVKKAR 16
| | | | | | | | | | | | | | | | | |
Db 293 NNATFFFKIDNVKKAR 308
RESULT 10
ID ABB78710
XX ABB78710 standard; Protein; 644 AA.
XX
AC ABB78710;
XX
XX 18-JUL-2002 (first entry)
DT
XX Human high molecular weight kininogen (HK) protein.
DE
XX Human; kininogen; high molecular weight kininogen; HK; D5 domain;
KW D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;
KW antiatherosclerotic; vasotropic; vulnary; tranquilliser; thrombolytic;

KW ophthalmological; gynaecological; antiulcer; antidiabetic; antiarthritic;
XX antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..18
FT /label= signal
FT Protein 19..644
FT /label= mature_human_high_molecular_weight_kininogen
FT Disulfide-bond 28..614
FT Disulfide-bond 83..94
FT Disulfide-bond 107..126
FT Disulfide-bond 142..145
FT Disulfide-bond 206..218
FT Disulfide-bond 229..248
FT Disulfide-bond 264..267
FT Disulfide-bond 328..340
FT Disulfide-bond 351..370
FT Domain 402..526
FT /label= D5_domain

XX WO200214369-A2.

PN 21-FEB-2002.

XX 24-JUL-2001; 2001WO-US23185.

XX 24-JUL-2000; 2000US-220194P.

XX (ATTE-) ATTENTION LLC.

XX Mazar AP, Juarez JC;

XX WPI; 2002-393611/42.

XX Novel human kininogen D5 domain polypeptides useful for treating
PT conditions associated with endothelial cell migration, proliferation,
PT invasion or angiogenesis, e.g. arthritis, macular degeneration, benign
PT hyperplasia

XX Disclosure; Fig 1B-E; 84pp; English.

XX The present invention describes an isolated polypeptide (I) that
CC corresponds to the D5 domain of human kininogen, or biologically active
CC peptide fragment, homologue or functional derivative, and which:
CC (a) inhibits angiogenesis; (b) binds to the D5 binding site on
CC endothelial cells (EC); (c) activates signalling pathways leading to the
CC introduction of apoptosis in EC; and/or (d) inhibits the signalling
CC pathway required for maintenance of EC viability. (I) has cytostatic,
CC antitumour, antiatherosclerotic, vasotropic, vulnerary, tranquiliser,
CC thrombolytic, ophthalmological, gynaecological, antiulcer, antidiabetic,
CC antiarthritic, antiangiogenic, antiapoptotic and endocrine activities.
CC An antibody (IX) specific for an epitope of (I) is useful for inhibiting
CC tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide
CC (II) or a dimeric or trimeric fusion polypeptide (III) can be used for
CC inhibiting EC migration, proliferation, invasion, or angiogenesis, or
CC for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical
CC composition (X) comprising (I), (II), or (III), can be used for treating
CC a subject having a disease or condition associated with undesired EC
CC migration, proliferation, invasion or angiogenesis. (I), (II), or (III)
CC can be used for isolating a D5 domain binding molecule from a complex
CC mixture and for isolating or enriching cells expressing D5 domain binding
CC sites from a cell mixture. The present sequence represents the human
CC high molecular weight kininogen (HK) protein, which is given in the
CC exemplification of the present invention.

XX Sequence 644 AA;

Query Match 100.0%; Score 84; DB 23; Length 644;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFFKIDNVKKAR 16
Db 293 NNATFFKIDNVKKAR 308
|||||

RESULT 11
AAW54336
ID AAW54336 standard; peptide; 26 AA.

XX AC AAW54336;

XX DT 30-JUL-1998 (first entry)

XX Bradykinin analogous peptide 19.

XX Inhibition; thrombin-induced platelet; prevention; platelet aggregation;
KW ADP-induced activation.

XX OS Synthetic.

XX PN WO9641640-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09940.

XX PR 09-JUN-1995; 95US-0000096.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Hasan AAK, Schmaier AH;

XX DR WPI; 1997-065304/06.

XX Inhibition of platelet activation and aggregation - by admin. of new
PT or known bradykinin analogues

XX Disclosure; Page 44; 73pp; English.

XX Administration of a peptide or multimer related to bradykinin or other
CC disclosed peptides and multimers can be used for the inhibition of
CC thrombin-induced platelets or other cells. They can also be used for
CC preventing platelet aggregation, or inhibiting ADP-induced activation.
CC This is useful to prevent arterial occlusions arising from coronary
CC thrombosis and stroke.

XX SQ Sequence 26 AA;

Query Match 92.9%; Score 78; DB 18; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NATFFKIDNVKKAR 16
Db 1 NATFFKIDNVKKAR 15
|||||

RESULT 12

ABG21105
ID ABG21105 standard; protein; 435 AA.

XX AC ABG21105;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #21096.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS85292.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX PS Claim 20; SEQ ID No 51464; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pdt_sequences.
XX SQ Sequence 435 AA;
Query Match 83.3%; Score 70; DB 22; Length 435;
Best Local Similarity 87.5%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 NNATFYFKIDNVKKAR 16
DB 297 NNAISYFKIDNVKKAR 312
RESULT 13
AAP40633
ID AAP40633 standard; Protein: 434 AA.
XX AC AAP40633;
XX DT 30-JUL-1992 (first entry)
XX DE Bradykinin protein precursor: type II (PKG146, PKG254).
XX KW Blood pressure; kininogen; probe..
XX FH Key Location/Qualifiers
XX PE 378..386
XX FT /label= bradykinin
XX FT 391..395
XX FT /note= "probe (AAN40241)-encoded sequence"
XX

PN JP59125896-A.
XX PD 20-JUL-1984.
XX PF 07-JAN-1983; 83JP-0000984.
XX PR 07-JAN-1983; 83JP-0000984.
XX PA (MITU) MITSUBISHI CHEM IND KK.
XX DR WPI; 1984-216122/35.
XX DR N-PSDB; AAN40314.
XX PT c-Dna fragment of protein precursor - used to code bradykinin
XX PS Disclosure; Fig 2; 6 pp; Japanese.
XX CC Bradykinin is a peptide consisting of nine amino acids. It has the
XX CC biological effect of decreasing blood pressure. Although kininogen
XX CC is known as a protein-precursor of bradykinin, its structure is unknown
XX CC because of the difficulty in collecting large enough samples of
XX CC kininogen for structural investigation.
XX SQ Sequence 434 AA;
Query Match 70.2%; Score 59; DB 5; Length 434;
Best Local Similarity 73.3%; Pred. No. 0.091;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 NNATFYFKIDNVKKA 15
DB 290 HGGTFYFKIDTVKKA 304
RESULT 14
AAB08553
ID AAB08553 standard; Peptide; 16 AA.
XX AC AAB08553;
XX DT 20-DEC-2000 (first entry)
XX DE Peptide identified from an origin of prepro-bradykinine.
XX KW Precursor peptide; polypeptide hormone; peptide identification.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "hydrogen attached"
XX FT Modified-site 16 /note= "amidated residue"
XX PN WO2000050636-A1.
XX PD 31-AUG-2000.
XX PF 24-FEB-2000; 2000WO-FR00460.
XX PR 25-FEB-1999; 99US-0257525.
XX PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Canara Ferrer YJA, Thureau C, Martinez J, Berge G, Goze C;
XX DR WPI; 2000-572101/53.
XX PT Identifying peptide with selected function, useful particularly for
XX PT C-amidated hormones, by screening database for combination of nucleic
XX PT acid and amino acid sequences -
XX

PS Claim 16; Page 20; 40pp; French.

XX The specification describes a method for identifying a peptide having

CC a particular function. The method comprises preparing a database of

CC polynucleotides and polypeptides of unknown functions, screening the

CC database for a combination of nucleotides or amino acids indicative of

CC the peptide with a particular function, and identifying polynucleotides

CC and proteins which contain the peptide. The method is used to identify

CC precursor peptides with an amidated C-terminus, especially polypeptide

CC hormones, for studying physiologically active substances. The present

CC sequence represents a peptide which was identified using the method of

CC the invention.

XX

SQ Sequence 16 AA;

Query Match 67.9%; Score 57; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0051;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 YFKIDNVKKAR 16

Db 1 YFKIDNVKKAR 11

|||||||

RESULT 15

ABG60077

ID ABG60077 standard; Protein; 235 AA.

XX

AC ABG60077;

XX

DT 30-JUL-2002 (first entry)

XX

DE Human DITHP polypeptide #135.

XX

KW Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;

KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;

KW inflammatory disorder; viral infection; bacterial infection; seizure;

KW fungal infection; parasitic infections; developmental disorder; breast;

KW endocrine disorder; metabolic disorder; neurological disorder; cervix;

KW gastrointestinal disorder; transport disorder; gene therapy; kidney;

KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;

KW thymus.

XX

OS Homo sapiens.

XX

PN WO200220754-A2.

XX

PD 14-MAR-2002.

XX

PF 29-AUG-2001; 2001WO-US27127.

XX

05-SEP-2000; 2000US-229747P.

PR

05-SEP-2000; 2000US-229748P.

PR

05-SEP-2000; 2000US-229749P.

PR

05-SEP-2000; 2000US-229750P.

PR

05-SEP-2000; 2000US-229751P.

PR

05-SEP-2000; 2000US-230583P.

PR

05-SEP-2000; 2000US-230585P.

PR

05-SEP-2000; 2000US-230514P.

PR

05-SEP-2000; 2000US-230515P.

PR

05-SEP-2000; 2000US-230517P.

PR

05-SEP-2000; 2000US-230518P.

PR

05-SEP-2000; 2000US-230519P.

PR

05-SEP-2000; 2000US-230595P.

PR

05-SEP-2000; 2000US-230597P.

PR

05-SEP-2000; 2000US-230598P.

PR

05-SEP-2000; 2000US-230599P.

PR

05-SEP-2000; 2000US-230610P.

PR

05-SEP-2000; 2000US-230865P.

PR

05-SEP-2000; 2000US-230988P.

PR

05-SEP-2000; 2000US-230951P.

PR

05-SEP-2000; 2000US-231163P.

PR

05-SEP-2000; 2000US-231167P.

XX (INCY-) INCYTE GENOMICS INC.

PA

XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;

PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;

PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;

PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;

PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;

XX WPI: 2002-383054/41.

DR N-PSDB; ABK71668.

XX

PT An isolated polynucleotide useful in diagnostics and therapeutics -

PS

XX Claim 29; Page 610-611; 686pp; English.

XX

CC The invention relates to human diagnostic and therapeutic (dithp)

CC polynucleotides and their associated polypeptides (DITHP polypeptides).

CC The sequences of the invention are used in the treatment and diagnosis of

CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers

CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, or

CC cervix), kidney, lung, ovary, pancreas, prostate, skin, spleen, testis, or

CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,

CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal

CC infections, parasitic infections, developmental disorders (e.g. anaemia,

CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),

CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders

CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,

CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal

CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders

CC (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences

CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention.

XX

SQ Sequence 235 AA;

Query Match 66.7%; Score 56; DB 23; Length 235;

Best Local Similarity 73.3%; Pred. No. 0.15;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 NNATFFFKIDNVKKA 15

Db 102 HNHLYFKIDTVKKA 116

|||||||

Search completed: March 13, 2003, 19:12:03

Job time : 43 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:57 ; Search time 15.3333 Seconds
(without alignments)
30.702 Million cell updates/sec

Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNAFFYFKIDNVKKAR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	117	1	Sequence 1, Appli
2	84	100.0	117	5	Sequence 1, Appli
3	78	92.9	26	4	Sequence 15, Appl
4	40	47.6	179	3	Sequence 3, Appli
5	38	45.2	608	1	Sequence 3, Appli
6	38	45.2	872	1	Sequence 2, Appli
7	37	44.0	149	4	Sequence 85, Appli
8	37	44.0	229	4	Sequence 3050, Ap
9	37	44.0	302	4	Sequence 14, Appl
10	37	44.0	305	4	Sequence 12, Appl
11	37	44.0	365	2	Sequence 2, Appli
12	36.5	43.5	514	1	Sequence 21, Appl
13	36.5	43.5	514	1	Sequence 21, Appl
14	36.5	43.5	514	1	Sequence 21, Appl
15	36	42.9	159	4	Sequence 5, Appli
16	36	42.9	167	4	Sequence 3554, Ap
17	35.5	42.3	320	1	Sequence 4, Appli
18	35.5	42.3	320	2	Sequence 4, Appli
19	35.5	42.3	320	2	Sequence 4, Appli
20	35.5	42.3	320	4	Sequence 4, Appli
21	35.5	42.3	358	1	Sequence 36, Appl
22	35.5	42.3	1171	1	Sequence 1, Appli
23	35	41.7	222	1	Sequence 12, Appl
24	35	41.7	240	1	Sequence 8, Appli
25	35	41.7	240	1	Sequence 12, Appl
26	35	41.7	240	2	Sequence 12, Appl
27	35	41.7	240	2	Sequence 12, Appl

Sequence 4, Appli
Sequence 12, Appl
Patent No. 5185441
Patent No. 5223394
Patent No. 5223394
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 10, Appl
Patent No. 5223394
Patent No. 5185441
Sequence 2, Appli
Sequence 31, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 64, Appl

ALIGNMENTS

RESULT 1

US-08-193-114B-1

Sequence 1, Application US/08193114B

Patent No. 5472945

GENERAL INFORMATION:

APPLICANT: Schmaier, Alvin H.

APPLICANT: Jiang, Yongping

TITLE OF INVENTION: Modulation of Blood

TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation

TITLE OF INVENTION: with Kininogen Fragment

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorgna &

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08193,114B

FILING DATE: 9 February 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Application

APPLICATION NUMBER: Serial No. 5472945 07/744,545

FILING DATE: 13 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-137 CII

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: NO. 5472945e

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: peptide

TOPOLOGY: linear

US-08-193-114B-1

Query Match 100.0%; Score 84; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 5.3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORGANISM: Feline herpesvirus-1
STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: Deduced sequence
OTHER INFORMATION: ICP18.5
US-08-911-321-3

Query Match 47.6%; Score 40; DB 3; Length 179;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NATFYFKIDNV 12
| | | : | |
Db 21 NTAFYFSVENV 31

RESULT 5
US-08-766-014-3
; Sequence 3, Application US/08766014
; Patent No. 5744312
; GENERAL INFORMATION:
; APPLICANT: Mamone, Joseph A.
; APPLICANT: Davis, Maria
; APPLICANT: Sha, Dan
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,014
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/104
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 608 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-014-3

Query Match 45.2%; Score 38; DB 1; Length 608;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKK 14
| | | : | |
Db 8 NKLEFFSLIDNIKK 21

RESULT 6
US-08-766-014-2
; Sequence 2, Application US/08766014
; Patent No. 5744312
; GENERAL INFORMATION:
; APPLICANT: Mamone, Joseph A.
; APPLICANT: Davis, Maria
; APPLICANT: Sha, Dan
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,014
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/104
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-014-2

Query Match 45.2%; Score 38; DB 1; Length 872;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKK 14
| | | : | |
Db 272 NKLEFFSLIDNIKK 285

RESULT 7
US-08-679-493A-85
; Sequence 85, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A

```
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-679-493A-85

Query Match          44.0%; Score 37; DB 4; Length 149;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YFKIDNVKAR 16
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Db 71 YFTSDNAKQAR 81

RESULT 8
US-09-134-001C-3050
; Sequence 3050, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3050
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3050

Query Match          44.0%; Score 37; DB 4; Length 229;
Best Local Similarity 87.5%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 FYFKIDNV 12
   |||| ||||
Db 174 FYFKEDNV 181

RESULT 9
US-09-282-305-14
; Sequence 14, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
```

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US-09-282-305-14

Query Match          44.0%; Score 37; DB 4; Length 302;
Best Local Similarity 53.3%; Pred. No. 93;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKA 15
   :|| | ||| :|
Db 38 DNALMYVKIDDQKLA 52

RESULT 10
US-09-282-305-12
; Sequence 12, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-12

Query Match          44.0%; Score 37; DB 4; Length 305;
Best Local Similarity 53.3%; Pred. No. 94;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKA 15
   :|| | ||| :|
Db 38 DNALMYVKIDDQKLA 52

RESULT 11
US-08-515-251A-2
; Sequence 2, Application US/08515251A
; Patent No. 5891677
; GENERAL INFORMATION:
; APPLICANT: GERLACH, GERALD F.
; APPLICANT: WILLSON, PHILIP J.
; APPLICANT: ROSSI-CAMPOS, AMALIA
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE OUTER
; TITLE OF INVENTION: MEMBRANE LIPOPROTEIN A AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/515,251A
; FILING DATE: 15-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,558
; FILING DATE: 05-NOV-1992
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; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0027.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-515-251A-2

Query Match 44.0%; Score 37; DB 2; Length 365;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NATFYFKIDN 11
| | | | |
Db 309 NGTLYSKIDN 318

RESULT 12
US-08-361-920-21
; Sequence 21, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5457046 No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE: 22-DEC-1994
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-939-21

Query Match 43.5%; Score 36.5; DB 1; Length 514;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 2 NATFYGSGSNENIDTTK 14
| | | | |
Db 287 NKTFYGSGSNENIDTTK 304

US-08-361-920-21
Query Match 43.5%; Score 36.5; DB 1; Length 514;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 2 NATFYGSGSNENIDTTK 14
| | | | |
Db 287 NKTFYGSGSNENIDTTK 304

RESULT 13
US-08-479-939-21
; Sequence 21, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5686593 No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE: 22-DEC-1994
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-939-21

Query Match 43.5%; Score 36.5; DB 1; Length 514;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 2 NATFYGSGSNENIDTTK 14
| | | | |
Db 287 NKTFYGSGSNENIDTTK 304
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RESULT 14

US-08-483-432-21
; Sequence 21, Application US/08483432
; Patent No. 5763254
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5763254o No. 5763254disk of No. 5763254th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,432
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-432-21

Query Match 43.5%; Score 36.5; DB 1; Length 514;

Best Local Similarity 50.0%; Pred. No. 2e+02; Mismatches 4; Indels 5; Gaps 1;

Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 2 NATFY-----FKIDNVKK 14

Db 287 NKTFYGPGSFNFDITKK 304

RESULT 15

US-09-230-670C-5
; Sequence 5, Application US/09230670C
; Patent No. 6384300
; GENERAL INFORMATION:
; APPLICANT: Greiner, Steffen
; APPLICANT: Universit Heidelberg
; APPLICANT: Rausch, Thomas
; APPLICANT: Krausgrill, Silke
; TITLE OF INVENTION: Invertase-Inhibitor
; FILE REFERENCE: 25048-13

; CURRENT APPLICATION NUMBER: US/09/230,670C
; CURRENT FILING DATE: 1998-04-05
; PRIOR APPLICATION NUMBER: PCT/EP97/04153
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-230-670C-5

Query Match 42.9%; Score 36; DB 4; Length 159;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 NATFYFKIDNVKKA 15

Db 142 NATFWKKMQYVRKS 155

Search completed: March 13, 2003, 19:14:32
Job time : 16.3333 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:12:07 ; Search time 14 Seconds
(without alignments)
52.677 Million cell updates/sec

Title: us-09-461-061a-10

Perfect score: 84
Sequence: 1 NNATYFKIDNVKKAR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	67.9	16	10	US-09-935-682-3
2	38	45.2	282	9	US-09-738-626-6055
3	38	45.2	585	10	US-09-815-242-4973
4	38	45.2	586	10	US-09-815-242-10580
5	37	44.0	281	12	US-10-010-901-40
6	37	44.0	302	10	US-09-883-720-14
7	37	44.0	305	10	US-09-883-720-12
8	37	44.0	359	10	US-09-815-242-13653
9	37	44.0	717	10	US-09-801-368-376
10	36	42.9	133	10	US-09-764-877-1463
11	36	42.9	400	10	US-09-815-242-5324
12	36	42.9	438	9	US-09-992-598-129
13	36	42.9	438	9	US-09-989-293A-129
14	36	42.9	438	9	US-09-989-735-129
15	36	42.9	438	9	US-09-990-444-129
16	36	42.9	438	9	US-09-989-730-129
17	36	42.9	438	9	US-09-990-436-129
18	36	42.9	438	9	US-09-991-181-129
19	36	42.9	438	9	US-09-993-687-129

20	36	42.9	438	9	US-09-989-734-129	Sequence 129, App
21	36	42.9	438	9	US-09-997-653-129	Sequence 129, App
22	36	42.9	438	9	US-10-174-590-110	Sequence 110, App
23	36	42.9	438	9	US-10-176-758-110	Sequence 110, App
24	36	42.9	438	9	US-10-175-737-110	Sequence 110, App
25	36	42.9	438	9	US-09-993-667-129	Sequence 129, App
26	36	42.9	438	9	US-10-173-706-110	Sequence 110, App
27	36	42.9	438	9	US-10-175-738-110	Sequence 110, App
28	36	42.9	438	9	US-10-175-752-110	Sequence 110, App
29	36	42.9	438	9	US-10-176-482-110	Sequence 110, App
30	36	42.9	438	9	US-10-176-757-110	Sequence 110, App
31	36	42.9	438	9	US-10-176-913-110	Sequence 110, App
32	36	42.9	438	9	US-10-180-552-110	Sequence 110, App
33	36	42.9	438	9	US-10-180-557-110	Sequence 110, App
34	36	42.9	438	9	US-09-990-438-129	Sequence 129, App
35	36	42.9	438	9	US-09-990-562-129	Sequence 129, App
36	36	42.9	438	9	US-09-997-428-129	Sequence 129, App
37	36	42.9	438	9	US-09-997-666-129	Sequence 129, App
38	36	42.9	438	9	US-10-173-700-110	Sequence 110, App
39	36	42.9	438	9	US-10-174-572-110	Sequence 110, App
40	36	42.9	438	9	US-10-174-579-110	Sequence 110, App
41	36	42.9	438	9	US-10-174-582-110	Sequence 110, App
42	36	42.9	438	9	US-10-174-588-110	Sequence 110, App
43	36	42.9	438	9	US-10-175-739-110	Sequence 110, App
44	36	42.9	438	9	US-10-175-740-110	Sequence 110, App
45	36	42.9	438	9	US-10-175-743-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-09-935-682-3
; Sequence 3, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified Nucleo
; TITLE OF INVENTION: Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 1999-02-25
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-682-3

Query Match 67.9%; Score 57; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YFKIDNVKKAR 16
| | | | | | | | | | | | | | | |
Db 1 YFKIDNVKKAR 11

RESULT 2
US-09-738-626-6055
; Sequence 6055, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO

APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOTEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6055
LENGTH: 282
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6055

Query Match 45.2%; Score 38; DB 9; Length 282;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 YFKIDNVK 14
|||:|:|:
DB 154 YFKVDVVK 162

RESULT 3
US-09-815-242-4973
; Sequence 4973, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4973
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4973

Query Match 45.2%; Score 38; DB 10; Length 585;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 NNATFFKIDNVKKAR 16
|||:|:|:
DB 343 NNATYLEVATVVKLAK 358

RESULT 4
US-09-815-242-10580
; Sequence 10580, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10580
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10580

Query Match 45.2%; Score 38; DB 10; Length 586;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 NNATFFKIDNVKKAR 16
|||:|:|:
DB 343 NNATYLEVATVVKLAK 358

RESULT 5
US-10-010-901-40
; Sequence 40, Application us/10010901
; Patent No. US20020098201A1
; GENERAL INFORMATION:
; APPLICANT: McFadden, Grant
; TITLE OF INVENTION: NOVEL MYXOMA GENES FOR IMMUNE MODULATION
; FILE REFERENCE: 50082/009002
; CURRENT APPLICATION NUMBER: US/10/010,901
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/615,041
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40

; LENGTH: 281
; TYPE: PRT
; ORGANISM: Myxoma Virus
US-10-010-901-40

Query Match 44.0%; Score 37; DB 12; Length 281;
Best Local Similarity 57.1%; Pred. No. 72;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFFKIDNVKKA 14
| | | | | | | | | |
Db 128 NVCTITFKINNVSK 141

RESULT 6

US-09-883-720-14
; Sequence 14, Application US/09883720
; Patent No. US2002022256A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44
; CURRENT APPLICATION NUMBER: US/09/883,720
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
US-09-883-720-14

Query Match 44.0%; Score 37; DB 10; Length 302;
Best Local Similarity 53.3%; Pred. No. 78;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFFKIDNVKKA 15
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Db 38 DNALMVVKIDDQKLA 52

RESULT 7

US-09-883-720-12
; Sequence 12, Application US/09883720
; Patent No. US2002022256A1
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44
; CURRENT APPLICATION NUMBER: US/09/883,720
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/282,305
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
US-09-883-720-12

Query Match 44.0%; Score 37; DB 10; Length 305;
Best Local Similarity 53.3%; Pred. No. 78;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFFKIDNVKKA 15
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Db 38 DNALMVVKIDDQKLA 52

RESULT 8

US-09-815-242-13653
; Sequence 13653, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13653
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13653

Query Match 44.0%; Score 37; DB 10; Length 359;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTFYFKIDNVKKA 15
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Db 324 THYFKLSEIEKA 335

RESULT 9

US-09-801-368-376
; Sequence 376, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368

; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 376
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-376

Query Match 44.0%; Score 37; DB 10; Length 717;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKAR 16
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DB 255 NNAEGLRIDNTEKDR 270

RESULT 10
US-09-764-877-1463
; Sequence 1463, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1463
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1463

Query Match 42.9%; Score 36; DB 10; Length 133;
Best Local Similarity 42.1%; Pred. No. 50;
Matches 8; Conservative 5; Mismatches 2; Indels 4; Gaps 1;

QY 2 NATFYFKID---NVKKAR 16
:| | :| | :| :| |
DB 67 HATAYKVDPPWNIQIAR 85

RESULT 11
US-09-815-242-5324
; Sequence 5324, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5324
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(400)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-5324

Query Match 42.9%; Score 36; DB 10; Length 400;
Best Local Similarity 35.7%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKK 14
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DB 308 NNGDTYFRVQTIEK 321

RESULT 12
US-09-992-598-129
; Sequence 129, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770

1	PRIOR APPLICATION NUMBER: 60/089538	
2	PRIOR FILING DATE: 1998-06-17	
3	PRIOR APPLICATION NUMBER: 60/089598	
4	PRIOR FILING DATE: 1998-06-17	
5	PRIOR APPLICATION NUMBER: 60/089599	
6	PRIOR FILING DATE: 1998-06-17	
7	PRIOR APPLICATION NUMBER: 60/089600	
8	PRIOR FILING DATE: 1998-06-17	
9	PRIOR APPLICATION NUMBER: 60/089653	
10	PRIOR FILING DATE: 1998-06-17	
11	PRIOR APPLICATION NUMBER: 60/089801	
12	PRIOR FILING DATE: 1998-06-18	
13	PRIOR APPLICATION NUMBER: 60/089907	
14	PRIOR FILING DATE: 1998-06-18	
15	PRIOR APPLICATION NUMBER: 60/089908	
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17	PRIOR APPLICATION NUMBER: 60/089947	
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19	PRIOR APPLICATION NUMBER: 60/089948	
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21	PRIOR APPLICATION NUMBER: 60/089952	
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23	PRIOR APPLICATION NUMBER: 60/090254	
24	PRIOR FILING DATE: 1998-06-22	
25	PRIOR APPLICATION NUMBER: 60/090349	
26	PRIOR FILING DATE: 1998-06-23	
27	PRIOR APPLICATION NUMBER: 60/090355	
28	PRIOR FILING DATE: 1998-06-23	
29	PRIOR APPLICATION NUMBER: 60/090429	
30	PRIOR FILING DATE: 1998-06-24	
31	PRIOR APPLICATION NUMBER: 60/090431	
32	PRIOR FILING DATE: 1998-06-24	
33	PRIOR APPLICATION NUMBER: 60/090435	
34	PRIOR FILING DATE: 1998-06-24	
35	PRIOR APPLICATION NUMBER: 60/090444	
36	PRIOR FILING DATE: 1998-06-24	
37	PRIOR APPLICATION NUMBER: 60/090445	
38	PRIOR FILING DATE: 1998-06-24	
39	PRIOR APPLICATION NUMBER: 60/090472	
40	PRIOR FILING DATE: 1998-06-24	
41	PRIOR APPLICATION NUMBER: 60/090535	
42	PRIOR FILING DATE: 1998-06-24	
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49	PRIOR APPLICATION NUMBER: 60/090676	
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55	PRIOR APPLICATION NUMBER: 60/090696	
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57	PRIOR APPLICATION NUMBER: 60/090862	
58	PRIOR FILING DATE: 1998-06-26	
59	PRIOR APPLICATION NUMBER: 60/090863	
60	PRIOR FILING DATE: 1998-06-26	
61	PRIOR APPLICATION NUMBER: 60/091360	
62	PRIOR FILING DATE: 1998-07-01	
63	PRIOR APPLICATION NUMBER: 60/091478	
64	PRIOR FILING DATE: 1998-07-02	
65	PRIOR APPLICATION NUMBER: 60/091544	

; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 42.9%; Score 36; DB 9; Length 438;

Best Local Similarity 43.8%; Pred. No. 1.6e+02;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 NNATEYFKIDNVKKAR 16

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Db 239 NMASLYGQDITKKLR 254

RESULT 13

US-09-989-293A-129

; Sequence 129, Application US/09989293A

; Patent No. US2002017164A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PlC66

; CURRENT APPLICATION NUMBER: US/09/989,293A

; PRIOR FILING DATE: 2001-11-20

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
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 ; PRIOR FILING DATE: 1998-06-02
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 ; PRIOR FILING DATE: 1998-06-02
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 ; PRIOR FILING DATE: 1998-06-03
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;	PRIOR APPLICATION NUMBER:	60/090690	
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;	PRIOR APPLICATION NUMBER:	60/090696	
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;	PRIOR APPLICATION NUMBER:	60/090862	
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;	PRIOR APPLICATION NUMBER:	60/090863	
;	PRIOR FILING DATE:	1998-06-26	
;	PRIOR APPLICATION NUMBER:	60/091360	
;	PRIOR FILING DATE:	1998-07-01	
;	PRIOR APPLICATION NUMBER:	60/091478	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091544	
;	PRIOR FILING DATE:	1998-07-01	
;	PRIOR APPLICATION NUMBER:	60/091519	
;	PRIOR FILING DATE:	1998-07-02	
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;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091633	
;	PRIOR FILING DATE:	1998-07-02	

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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;

Query Match      42.9%  Score
Best Local Similarity 43.8%  Pred.
Matches 7; Conservative

Qy      1  NNATFYKIDNVKKAR 16
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Db      239  NNASLYGOLDFTKKLR 254

RESULT 14
US-09-989-735-129
; Sequence 129, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Justin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secured and Tra
; TITLE OF INVENTION: Acids Encoding
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/98
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-07-07

Query Match 42.9%; Score 36; DB 9; Length 438;
Best Local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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RESULT 15

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Search completed: March 13, 2003, 19:15:02
 Job time : 16 secs

Query Match 42.9%; Score 36; DB 9; Length 438;
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 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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